

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 26, 2003, 06:48:54 ; Search time 40.2691 Seconds
(without alignments)
1899.367 Million cell updates/sec

Title: US-09-225-502-6

Perfect score: 3054

Sequence: 1 MAFGRWRPPPPPLLLLLLV.....AEEFKLXQEKHVDYTLNLA 574

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 101002.*

1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
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9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
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15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
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20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3001	98.3	570	22	Human membrane or
2	2883	94.4	541	20	Amino acid sequenc
3	1744	57.1	582	22	Amino acid sequenc
4	1742	57.0	582	21	Hydrophobic domain
5	1742	57.0	582	21	Human isomerase ho
6	1606	52.6	388	20	Amino acid sequenc
7	1399	45.8	441	20	Amino acid sequenc
8	1354	44.3	434	21	Human pancreatic c
9	831	27.2	166	23	Human ovarian anti
10	760	24.9	1241	22	Novel human diagno

11	743	24.3	366	21	AA571114	Human prostate can
12	737	24.1	316	20	AAV23884	Amino acid sequenc
13	651	21.3	127	22	AA05027	Human polypeptide
14	309	10.1	216	22	AB64697	Drosophila melanog
15	297	9.7	131	22	AAU87239	Novel central nerv
16	291	9.5	129	22	AAU87542	Novel central nerv
17	291	9.5	129	22	AAU87542	Human polypeptide
18	291	9.5	129	22	AAU19949	Human human calciu
19	270	8.8	138	22	AB69722	Drosophila melanog
20	268	8.8	219	20	AAW88556	Secreted protein e
21	268	8.8	219	22	AB50323	Human secreted p
22	268	8.8	222	21	AAU84429	Human PRO1304 prot
23	268	8.8	222	21	AAU84429	Amino acid sequenc
24	268	8.8	222	21	AAU84429	Human PRO1304 (UNQ
25	268	8.8	222	21	AAU84429	Protein of the inv
26	268	8.8	222	22	AAU84429	Human PRO1304 prot
27	259.5	8.5	159	21	AAU10995	Arabidopsis thalia
28	259.5	8.5	163	21	AAU10995	Arabidopsis thalia
29	256	8.4	211	20	AAU1706	Human PRO381 prote
30	256	8.4	211	20	AAU1706	Polypeptide fragme
31	256	8.4	211	21	AAU1706	Human PRO381 (UNQ3
32	256	8.4	211	21	AAU1706	Human PRO381 prote
33	256	8.4	211	21	AAU1706	Human PRO381 prote
34	256	8.4	211	21	AAU1706	Human secreted pro
35	256	8.4	211	22	AAU12363	Human PRO381 polyp
36	256	8.4	211	22	AAU12363	Human PRO381 prote
37	256	8.4	211	22	AAU12363	Human PRO381 prote
38	253	8.3	146	21	AAU12363	Arabidopsis thalia
39	253	8.3	152	21	AAU12363	Arabidopsis thalia
40	253	8.3	152	21	AAU12363	Arabidopsis thalia
41	249.5	8.2	186	20	AAU1459	Polypeptide fragme
42	247	8.1	146	21	AAU1459	Arabidopsis thalia
43	247	8.1	152	21	AAU1459	Arabidopsis thalia
44	247	8.1	152	21	AAU1459	Arabidopsis thalia
45	245.5	8.0	163	23	ABG05730	Human DITHP polype

ALIGNMENTS

RESULT 1

AA88320
ID AAB88320 standard; Protein; 570 AA.

AC AAB88320;

XX 23-MAY-2001 (first entry)

DT Human membrane or secretory protein clone P8EC0007.

DE Human; secretory protein; membrane protein; vaccine; gene therapy;

KW rheumatoid arthritis; diabetes.

XX Homo sapiens.

OS EP1067182-A2.

PN 10-JAN-2001.

PD 07-JUL-2000; 2000EP-0114090.

PF 08-JUL-1999; 99JP-0194179.

PR 11-JAN-2000; 2000JP-0118775.

PR 02-MAY-2000; 2000JP-0183766.

XX (HELI-) HELIX RES INST.

PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;

XX WPI; 2001-093989/11.

DR N-PSDB; AAF93747.

XX Nucleic acids encoding secretory proteins/membrane proteins, useful in

gene therapy or as candidate target molecules in drug development -
Claim 1; SEQ ID 8; 609pp + CD ROM; English.

This invention relates to nucleic acid sequences AAF93744 - AAF93916 which encode human secretory or membrane proteins represented by AAB88317 - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the invention. The invention also includes methods for the production of antibodies directed against the proteins, and cDNA sequences, which can be used in vaccines. The polynucleotide sequences can be used in gene therapy. The polynucleotide sequences and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate secretory protein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The polypeptides may be used as antigens in the production of antibodies against them and in assays to identify modulators (agonists and antagonists) of expression and activity. The antibodies and antagonists may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbent assay (ELISA). Examples of diseases which may be treated include rheumatoid arthritis and diabetes.

Query Match 98.3%; Score 3001; DB 22; Length 570;
Best Local Similarity 98.9%; Pred. No. 1.7e-282;
Matches 562; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

1 MAFRGWRPPPPPLLLLLWVTGQAPVAGLSDAELQIERRFVDPDECPTVRSGDFVRYH 60
1 MAFRGWRPPPPPLLLLLWVTGQAPVAGLSDAELQIERRFVDPDECPTVRSGDFVRYH 60
61 YVGFDPGOKSSYDRDSTNFVKGQLTGMQALVGMVNRERRFKIPPKLAYNE 120
61 YVGFDPGOKSSYDRDSTNFVKGQLTGMQALVGMVNRERRFKIPPKLAYNE 120
121 RVSGVIPPNSVLFHFDVLLMDIWNSSDQVQIHTYFKPPSPCRITQVSDFRVHYNGTFLDG 180
121 RVSGVIPPNSVLFHFDVLLMDIWNSSDQVQIHTYFKPPSPCRITQVSDFRVHYNGTFLDG 180
181 TLFDSHNRMTYDTPYVIGWMLIPGMDKGLLGMVCGEKRIITIPPLAYGEDGDKIIPG 240
181 TLFDSHNRMTYDTPYVIGWMLIPGMDKGLLGMVCGEKRIITIPPLAYGEDGDKIIPG 240
241 QASLVDFVALLDLHNPDKSISTENKVPENCERISQSGDFLTHYNGTLLDGTFLDSSYS 300
241 QASLVDFVALLDLHNPDKSISTENKVPENCERISQSGDFLTHYNGTLLDGTFLDSSYS 300
301 RNRFTDTYIGQYVTPGMDGLLVCIGEKRIIVPPHLYGEGRGNIIPGSVAVLFDIH 360
301 RNRFTDTYIGQYVTPGMDGLLVCIGEKRIIVPPHLYGEGRGNIIPGSVAVLFDIH 360
361 VIDFHNPSDSISITSHYKPPDCSVLSKGDYLYKHYNASLLDGTLLDSTWNLGKTYNIVL 420
361 VIDFHNPSDSISITSHYKPPDCSVLSKGDYLYKHYNASLLDGTLLDSTWNLGKTYNIVL 420
421 GSGQVVLGMDGLRMCVCGEKRTV1IPPHLYGEGAGVGEVPGSAVLVFDIELELVAGL 480
421 GSGQVVLGMDGLRMCVCGEKRTV1IPPHLYGEGAGVGEVPGSAVLVFDIELELVAGL 480
481 PEGYMFVWNGEVSNIPEIDKNGEVLLEEFSEYIIHAQVASKGKLAPGDAELIVKN 540
481 PEGYMFVWNGEVSNIPEIDKNGEVLLEEFSEYIIHAQVASKGKLAPGDAELIVKN 540
541 MFTNDRNGDGKVTAEFFKLKQDEAKHD 568

Db 541 MFTNDRNGDGKVTAEFFKLKQDEAKHD 568

RESULT 2
AAV23886
ID AAV23886 standard; Protein; 541 AA.
XX
AC AAV23886;
XX
DT 21-SEP-1999 (first entry)
XX
DE Amino acid sequence of a FK506 binding protein.
XX
KW Human; FK506 binding protein; FKBP65; immune system disorder;
KW immune cell; hematopoietic cell disorder; thrombolytic activity;
KW blood coagulation disorder; blood platelet disorder; wound;
KW heart attack; stroke; scarring; autoimmune disorder; allergic reaction;
KW asthma; allergic asthma; respiratory problem; anaphylaxis;
KW hypersensitivity; blood group incompatibility; organ rejection;
KW graft versus host disease; inflammatory condition;
KW ischemia-reperfusion injury; endotoxin lethality; arthritis;
KW complement-mediated hyperacute rejection; nephritis; lung injury;
KW inflammatory bowel disease; Crohn's disease; infection.
XX
OS Homo sapiens.
XX
PN W09935160-A1.
XX
PD 15-JUL-1999.
XX
PF 06-JAN-1999; 99WO-US00120.
XX
PR 09-JAN-1998; 98US-0070875.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Moore PA, Ruben SM, Wei Y;
XX
PI WPI; 1999-430382/36.
XX
DR N-PSDB; AAX86147.
XX
PT New nucleic acids encoding human FK506 binding proteins
XX
PS Claim 12; Fig 3; 87pp; English.
XX
CC The present sequence represents human FK506 binding protein 65 (FKBP65).
CC The polypeptide or polynucleotide may be useful in treating deficiencies
CC or disorders of the immune system, by activating or inhibiting the
CC proliferation, differentiation, or mobilization (chemotaxis) of immune
CC cells. They may be useful in treating or detecting deficiencies or
CC disorders of hematopoietic cells, to increase differentiation and
CC proliferation of hematopoietic cells including the pluripotent stem
CC cells, in an effort to treat those disorders associated with a decrease
CC in certain types of hematopoietic cells. They can be used to modulate
CC hemostatic or thrombolytic activity, e.g. an increase can treat blood
CC coagulation disorders, blood platelet disorders or wounds resulting from
CC trauma, surgery or other causes, or a decrease can treat heart attacks,
CC strokes or scarring. They can also treat autoimmune disorders, allergic
CC reactions and conditions such as asthma (particularly allergic asthma) or
CC molecule, or blood group incompatibility, organ rejection or graft versus
CC host disease, inflammatory conditions, both chronic and acute, including
CC inflammation associated with infection, ischemia-reperfusion injury,
CC endotoxin lethality, arthritis, complement-mediated hyperacute rejection,
CC nephritis, cytokine or chemokine induced lung injury, inflammatory bowel
CC disease, or Crohn's disease. They can also be used to treat viral,
CC bacterial, fungal and parasitic infections.
XX
SQ Sequence 541 AA;
Query Match 94.4%; Score 2883; DB 20; Length 541;
Best Local Similarity 100.0%; Pred. NO. 4.7e-271;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFRGWPPPPPLLLLLLWVTGQAAPVAGLSDAELQIERFVDECPRTVRSQDFVRYH 60
Db 1 MAFRGWPPPPPLLLLLLWVTGQAAPVAGLSDAELQIERFVDECPRTVRSQDFVRYH 60
QY 61 YVGTFFDQKQFSSYDRDSTFNVFVGKQLITGMDQALVGMVNERFVKIPPKLAYGNE 120
Db 61 YVGTFFDQKQFSSYDRDSTFNVFVGKQLITGMDQALVGMVNERFVKIPPKLAYGNE 120
QY 121 RVSGVIPPNSVLHFDVLLMDIWNSEDQVQIHTYKPPSCPTIOVSDRVRYHNGTFLDG 180
Db 121 RVSGVIPPNSVLHFDVLLMDIWNSEDQVQIHTYKPPSCPTIOVSDRVRYHNGTFLDG 180
QY 181 TLFSSSHNRMTYDTYVIGWMLIPGMDKGLGCMVGEKRIITIPPLAYGEDGDKOIPG 240
Db 181 TLFSSSHNRMTYDTYVIGWMLIPGMDKGLGCMVGEKRIITIPPLAYGEDGDKOIPG 240
QY 241 QASLVFDVALLDLHNPKDSISIEKVPENCERISQSGDFTLYHYNGTLLDGTLPDSSYS 300
Db 241 QASLVFDVALLDLHNPKDSISIEKVPENCERISQSGDFTLYHYNGTLLDGTLPDSSYS 300
QY 301 RNRTEFTYIGQYVTPGMDGELGVCIGEKXIVVPPHLYGEEGRGNIPGSAVLVFDIH 360
Db 301 RNRTEFTYIGQYVTPGMDGELGVCIGEKXIVVPPHLYGEEGRGNIPGSAVLVFDIH 360
QY 361 VIDFNPDSISITSHYKPPDCSVLSKKGDLKYHYNASLLDGTLLDSTWNLGKTYNIVL 420
Db 361 VIDFNPDSISITSHYKPPDCSVLSKKGDLKYHYNASLLDGTLLDSTWNLGKTYNIVL 420
QY 421 GSGQVVLGMDGLREMCVGEKRTVIPPPLHYGEAGVGEVPGSAVLVFDIEXLELVAGL 480
Db 421 GSGQVVLGMDGLREMCVGEKRTVIPPPLHYGEAGVGEVPGSAVLVFDIEXLELVAGL 480
QY 481 PGYMFVWNGEVSPLFEEDKNGEVLLEBFSEYIHAQVASKGKAPGFAELIVKN 540
Db 481 PGYMFVWNGEVSPLFEEDKNGEVLLEBFSEYIHAQVASKGKAPGFAELIVKN 540
QY 541 M 541
Db 541 M 541
RESULT 3
AAG79226
ID AAG79226 standard; Protein; 582 AA.
AC AAG79226;
DT 03-JAN-2002 (first entry)
DE Amino acid sequence of neurotrophic factor expression-inducing agent.
KW Human; neurotrophic factor; PSEC56; nerve growth factor;
KW neurite outgrowth; neural disease; dementia; cerebral embolism;
KW spinal injury; peripheral nerve disease.
OS Homo sapiens.
XX W0200173024-A1.
XX 04-OCT-2001.
XX 30-MAR-2001; 2001WO-JP02768.
XX 31-MAR-2000; 2000JP-0101300.
XX (HELI-) HELIX RES INST.
XX (WELF-) WELFIDE CORP.
XX Mitumori C, Morikawa N, Hayashi K, Nagahari K, Ota T, Hio Y;
XX Nishikawa T, Isogai T, Kawasaki M, Hashimoto K, Kishimoto T;
XX WPI; 2001-616501/71.
DR

N-PSDB; AAI65835.
Neurotrophic factor expression-inducing agent, applicable in developing drugs for neural diseases e.g. dementia, cerebral embolism, spinal injury and peripheral nerve diseases by screening their regulatory effect
Example 1; Page 34-38; 42pp; Japanese.
The present sequence represents a human neurotrophic factor expression-inducing agent. The polypeptide is designated PSEC56. The PSEC56 protein is used to increase nerve growth factor providing neurite outgrowth effect, which is applicable in developing drugs for neural diseases e.g. dementia, cerebral embolism, spinal injury and peripheral nerve diseases, with use of PSEC56 as the neurotrophic factor expression-inducing agent which can be applied in a system to study induction and secretion mechanism of neurotrophic factor.
Sequence 582 AA;
Query Match 57.1%; Score 1744; DB 22; Length 582;
Best Local Similarity 56.4%; Pred. No. 2.7e-160; Indels 22; Gaps Matches 326; Conservative 99; Mismatches 131;
QY 10 PP-----PLLLLLWVT-----GQAAPVAGLSDAELQIERFVDECPRTVRSQD 55
Db 6 PPSHLLRLPLQLLLLLLVQAVRGRLGRASPAGPLED--VVIERYHIPRACPREVQMGD 63
QY 56 FVRHYVGTFFDQKQFSSYDRDSTFNVFVGKQLITGMDQALVGMVNERFVKIPPKL 115
Db 64 FVRHYNGTFFDQKQFSSYDRNTLVAIVVGVRLLITGMDRGLMGCMVNERRLIVPPHL 123
QY 116 AYCNERVSGVTPNSVLHFDVLLMDIWNSEDQVQIHTYKPPSCPTIOVSDRVRYHNG 175
Db 124 GYGSIGLAGLIPDATALYFDVLLVWNKEDTVQSTLLRPHPCPRWQDGFVRYHNG 183
QY 176 TFLDGTLPDSSSHNRMTYDTYVIGWMLIPGMDKGLGCMVGEKRIITIPPLAYGEDG 235
Db 184 TLLDGTFFDTSYKGGTYDTYVSGWMLIKGMDQGLGCMVGEKRIITIPPLAYGEKGYG 243
QY 236 KDIPQASLVFDVALLDLHNPKDSISIEKVPENCERISQSGDFTLYHYNGTLLDGTLP 295
Db 244 TVTIPQASLVFVHLLIDVHNPKDAVQLETLPLPGCVRRAGAGDFRYHYNGSLMDGTLP 303
QY 296 DSSYSNRNRTFTYIGQYVTPGMDGELGVCIGEKXIVVPPHLYGEEGRGN-IPGSAV 354
Db 304 DSSYSNRNHTYNTYIGQYVTPGMDQGLQACMGERRITIPPLAYGENTGDKIPGSAV 363
QY 355 LVFDIHVIDFHNPSDSISITSHYKPPD-CSVLKSGDYLKYHYNASLLDGTLLDSTWNLG 413
Db 364 LIFNVHVIDFHNPADVVEIRTLSPSETCNETTKLGDVRYHYNCSLLDGTQLFTSHDYG 423
QY 414 KTYNVILGSGQVVLGMDGLREMCVGEKRTVIPPPLHYGEAGVGEVPGSAVLVFDIEX 473
Db 424 APOEATLGANKVIEGLDTGLQCMVGEKRLQIVPPHLAGESGARG-VPGSAVLLEFVEL 482
QY 474 LELVAGLPEGYMFVWNGEVSPLFEEDKNGEVLLEBFSEYIHAQVASKGKAPGFD 533
Db 483 VSREDGLPTGYLFWHKKDPPANLFDMDLNDKGEVPEEPSTFIKAQVSEKGRMLPQD 542
QY 534 AELIVKNMFTNQDRNGDKVTAEEFKL---XDOEAKHD 568
Db 543 PEKTIGDMFQNDQNDGKITVDLKLKSDDEDEERVHE 580
RESULT 4
AAB12128
ID AAB12128 standard; Protein; 582 AA.
AC AAB12128;
XX AAB12128;
XX 02-FEB-2001 (first entry)
XX

Hydrophobic domain protein from clone HPO2991 isolated from KB cells.

Human; secreted protein; membrane protein; hydrophobic domain; proliferation control; differentiation induction; material transport; biophysics; signal receptor; ion channel; transporter; immunostimulant; immunosuppressant; haematopoiesis regulator; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; autoimmune disease; Alzheimer's disease; Parkinson's disease; cancer.

Homo sapiens.

WO200029448-A2.

25-MAY-2000.

17-NOV-1999; 99WQ-JP06412.

17-NOV-1998; 98JP-0326255.

22-DEC-1998; 98JP-0364315.

16-MAR-1999; 99JP-0069811.

27-APR-1999; 99JP-0119299.

19-MAY-1999; 99JP-0138169.

(SAGA) SAGAMI CHEM RES CENT.

(PROT-) PROTEGENE INC.

Kato S, Kimura T;

WPI; 2000-387753/33.

N-PSDB; AAA62001, AAA62011.

Proteins comprising hydrophobic regions, such as secretory and membrane

activities e.g. immunomodulatory, antiinflammatory, chemokinetic,

hemostatic, thrombolytic -

Claim 1; Page 230-232; 410pp; English.

Secretory proteins play important roles in the proliferation control, the differentiation induction, the material transport and the biophysics of cells. Membrane proteins have important roles as signal receptors, ion channels and transporters. The present sequence is a human protein which has at least one hydrophobic domain. This protein may be a secretory or a membrane protein. The present protein may have cytokine and cell proliferation/differentiation activity, immune stimulating or suppressing activity, haematopoiesis activity, tissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, anti-inflammatory activity and tumour inhibition activity. The present protein could therefore be used for treatment of autoimmune disease, Alzheimer's disease, Parkinson's disease, and cancer.

Sequence 582 AA;

Query Match 57.0%; Score 1742; DB 21; Length 582;

Best Local Similarity 56.4%; Pred No. 4.3e-160;

Matches 326; Conservative 99; Mismatches 131; Indels 22; Gaps 7;

QY 10 PP-----PLLLLLLWMT-----GQAPVAGLGSDAELQIERFVPECPRTVRSQD 55

DB 6 PPSHLLRLFLQLLLLVVQAVGRGLGRASPAGGPLED--VVIERVHI PRACPREVQMGD 63

QY 56 FRYHYVGTFFDQKFDSSYDRDSTNFVFGKQLITGMDQALVGMVNERBFRVKTIPPKL 115

DB 64 FRYHYNGTFDQKFDSSYDRDNTLVAIVVGVRLITGMDRGLMGMVNERRLVPPHL 123

QY 116 AYGNERVGVIPNSVHFDVLLMDIWNSEDQVQIHTYFKPSCPRTIQVDFRVHYNG 175

DB 124 GYSGISGLAGLIPDATALYFDVLLDVNNKEDTVQVSTLLRPHCPRNVDGDFRVHYNG 183

QY 176 TFLDGTFLPSSSHRMKTYDTYVIGLWLPQMDKGLGMGVGKRIITIPPELAYGSDGQ 235

DB 184 TLJDTGSFDTYSKGTYYTVVGSGLWIKGMDQGLGMCFGERKRIIPPELAYGKGYG 243

QY 236 KDIPQASLVEDVALLDLHNPKDSISITSHYKPPD--CSVLKSGDYLYKHYNASLLDGTLLDSTWNLG 295

DB 244 TVIPQASLVEPHVLLIDVHNPKDAVQLETLPLPGCVRAGAGDFMRHYHNGSLMDGTFLF 303

QY 296 DSSYSRNRFTFTYIQGGVVIIPGMDGLGVCIGEKXIVVPPHLYGYGEGRGN--IPGSVA 354

DB 304 DSSYSRNRHTYTYIQGGVVIIPGMDGLGVCIGEKXIVVPPHLYGYGEGRGN--IPGSVA 363

QY 355 LVFDIHVIDFHNPSDSISITSHYKPPD--CSVLKSGDYLYKHYNASLLDGTLLDSTWNLG 413

DB 364 LIFNVHVIDFHNPAVVEIRTLRSPSETCNETTKGLDFVRHYNCSLLDGTQLTSHDYG 423

QY 414 KTYNIVLGSQGVWLGMDGLFREMCMGKRTVIIIPPHLYGYGAGVDGVPVGSVAIVFOIE 473

DB 424 APOEATLGANKRVIEGLDTGLQGMVGERQLIVPPLAHGSGARG--VPGSAVLLFVEL 482

QY 474 LELVAGLPEGVNTWNGEVSPLFEEDKONGEVLLEEFSEYTHAQSAGKGLAPGFD 533

DB 483 VSREDGLPTGYLFWHKDPPANLFDMDLNKDGVEVPPEEFSTFIKAQVSEKGRIMPQD 542

QY 534 AELIVQNMFTNDRNGDGKVTAEKFL---XDOEAKHD 568

DB 543 PEKTIGDMFQNDNRQDKITVDLKLKSDDEERVHE 580

RESULT 5

AAV52294

ID AAV52294 standard; Protein; 582 AA.

AC AAV52294;

DT 09-FEB-2000 (first entry)

XX Human isomerase homologue-1 (HIH-1).

XX Human isomerase homologue; HIH; FKBP65; PPIase;

XX peptidyl-prolyl cis/trans isomerase; FK506; rapamycin;

XX signalling pathway; T-cell; cancer; leukaemia; testicular cancer;

XX melanoma; immune disorder; asthma; atherosclerosis; diagnosis; treatment;

XX prevention; detection; agonist; antagonist; expression; activity;

XX antibody; apoptosis; gene therapy; genetic immunisation; vaccine.

XX Homo sapiens.

Key Location/Qualifiers

Region 210..238

FT. /note= "FKBP-type peptidyl-prolyl cis/trans isomerase signature sequence"

FT Domain 555..567

FT /note= "EF-hand calcium-binding domain"

FT Region 579..582

FT /note= "Endoplasmic reticulum targeting sequence"

FT Modified-site 70

FT /note= "N-glycosylated"

FT Modified-site 72

FT /note= "Phosphorylated by casein kinase II"

FT Modified-site 81

FT /note= "Phosphorylated by casein kinase II"

FT Modified-site 83

FT /note= "Phosphorylated by tyrosine kinase"

FT Modified-site 100

FT /note= "Phosphorylated by casein kinase II"

FT Modified-site 182

FT /note= "N-glycosylated"

FT Modified-site 184

FT /note= "Phosphorylated by casein kinase II"

FT Modified-site 189

FT /note= "Phosphorylated by casein kinase II"

FT Modified-site 294

FT /note= "N-glycosylated"

FT Modified-site 296

FT /note= "Phosphorylated by casein kinase II"

FT Modified-site 301 /note= "Phosphorylated by casein kinase II"
 FT Modified-site 310 /note= "N-glycosylated"
 FT Modified-site 342 /note= "phosphorylated by cAMP/cGMP-dependent protein kinase"
 FT Modified-site 352 /note= "N-glycosylated"
 FT Modified-site 391 /note= "Phosphorylated by casein kinase II"
 FT Modified-site 393 /note= "N-glycosylated"
 FT Modified-site 395 /note= "Phosphorylated by protein kinase C"
 FT Modified-site 407 /note= "N-glycosylated"
 FT Modified-site 409 /note= "Phosphorylated by casein kinase II"
 FT Modified-site 418 /note= "Phosphorylated by casein kinase II"
 FT Modified-site 484 /note= "Phosphorylated by casein kinase II"
 FT Modified-site 546 /note= "Phosphorylated by casein kinase II"
 FT Modified-site 563 /note= "Phosphorylated by casein kinase II"
 US5989860-A.
 23-NOV-1999.
 12-DEC-1997; 97US-0989386.
 12-DEC-1997; 97US-0989386.
 (INCY- INCYTE PHARM INC.
 Corley NC, Shah P, Bandman O, Hillman JL, Guegler KJ;
 WPI; 2000-022783/02.
 N-PSDB; AA232925.
 Nucleic acids encoding human isomerase homologs useful for the prevention, diagnosis and treatment of cancers and immune disorders -
 Claim 1; Fig 1; 49pp; English.
 This sequence represents human isomerase homologue-1 (HIH-1).
 Nucleotides encoding HIH-1 were first identified in an ovarian tumour cDNA library, the cDNA encoding this sequence being a consensus. HIH-1 is also expressed in other cancerous tissues, lymph nodes, inflamed colon, and synovium. HIH-1 has chemical and structural homology with mouse FKBP5, sharing 88% identity as well as the isomerase signature sequence, the endoplasmic reticulum targeting sequence and many of the potential phosphorylation sites. FKBP5 (FK506 binding proteins) are a family of peptidyl-prolyl cis/trans isomerases (PPIases) which catalyse the cis to trans isomerisation of certain proline imidic bonds in proteins. FKBP5 can bind the potent immunosuppressants FK506 and rapamycin, inhibiting PPIase activity and thus blocking signalling pathways in T-cells. The expression pattern of HIH-1 and its homology with FKBP5 indicate that it plays a role in cancers (e.g., leukaemia, testicular cancer and melanoma) and immune disorders (e.g., asthma and atherosclerosis). HIH proteins, and the nucleotides that encode them, may be used for the diagnosis, treatment or prevention of such diseases. HIH proteins may be used to identify agonists and antagonists of expression and/or activity, and to raise antibodies. The antibodies and antagonists may be used to downregulate expression and/or activity and increase apoptosis, and the antibodies may also be used in detection of HIH proteins and diagnosis of associated diseases. HIH nucleotides may be used in gene therapy or in the production of recombinant protein either in vitro, or in vivo (e.g., as part of genetic immunisation protocol).

XX SQ Sequence 582 AA;
 Query Match 57.0%; Score 1742; DB 21; Length 582;
 Best Local Similarity 56.4%; Pred. No. 4.3e-160;
 Matches 326; Conservative 99; Mismatches 131; Indels 22; Gaps 7;
 Qy 10 PP-----PLLLLLLWT-----GQAPVAGLSGDAELQIRRFVDPDCPRVRSQD 55
 Db 6 PPSHLLFLPLQLLLLVVQVGRGLGRASPAGGLE--VVIERYHIIPRACPREVQMGD 63
 Qy 56 FVRHYVGTFFDGOKFSSYDRDSTFNFGKGLITGMDQALVGMCMYNNRRFVKIPKL 115
 Db 64 FVRHYNGTFFDGKFKFSSYDRNTLVAIVGVGRLLITGMDGLMCMYNNRRLLVPPHL 123
 Qy 116 AYGNERSGVIPPNVSLHFDVLLMDIWNSEDOVQHTVFKPPSCPTTQVDFVRYHYNG 175
 Db 124 GYGSIGLAGLIPPDATLYFDVLLDMNKEDTVQSTLLRPPHCPRMVQDGFVRYHYNG 183
 Qy 176 TFLDGTFLDSSHNRMKTYDYVYGIGWLLIPGMDKGLGCMVGEKRIITPPFLAYGEDGDG 235
 Db 184 TLLDGTSTFDTYSKGGTYDYVVGSLWGLINGMDQGLGCMVGEKRIITPPFLAYGEKYG 243
 Qy 236 KDIPQASLVFDVALLDHNPKDSISIEKNVVPENCERISQSGDFLTTHYNGTLLDGTLP 295
 Db 244 TVIPQASLVFHVLLIDVHNPKDAVQLETLELPPGCVRRAGAGDFMRVHYNGSLMDGTLF 303
 Qy 296 DSSYRNRTFTDYIGQYVPGMDGELLGVCIGEXXIVVPPHGLGYGEGRGN-IPGSV 354
 Db 304 DSSYRNHTYNTYIGQYIIPGMDQGLGCMVGEKRIITPPHLAGESGARG-VFSAVLLFEVL 363
 Qy 355 LVFDTHVIDFHNPSDSISITSHYKPD-CVLSKKGDKYLYHYNASLLDGTLLDSTWNLG 413
 Db 364 LIFNVHVIDFHNPAVVEIRTLSPSETCNETTKLGDVRYHYNCSSLDTQLFTSHDYG 423
 Qy 414 KTYNIVLGSQVVLGMDGLREMCVGEKRTIIPPHGLGYGEAGDGEVPGSAVLVFDIEX 473
 Db 424 APQEAATLGANKVTEGLDTGLQGMVGERQLIVPPHLAGESGARG-VFSAVLLFEVL 482
 Qy 474 LELVAGLPGYMPFVNGEVSPLFEIDKNGEVLLEFSEYIHAQVAGKGLAPGFD 533
 Db 483 VSREDGLPTGYLFVWHKPPANLFDMDLNKGGEVPEEFSTFIKAQVSEKGRLLMPGD 542
 Qy 534 AELIVKNMFTNDRNGDGKVTAEFFKL---XDOEAKHD 568
 Db 543 PEKTIGDMFQNDQNDQDKITVDELKLSDEDEERVHE 580
 RESULT 6
 ID AAY23887
 XX AAY23887 standard; Protein; 388 AA.
 AC AAY23887;
 DT 21-SEP-1999 (first entry)
 XX Amino acid sequence of a FK506 binding protein 65.
 XX Human; FK506 binding protein; FKBP5; immune system disorder;
 XX Immune cell; hematopoietic cell disorder; thrombolytic activity;
 XX Blood coagulation disorder; blood platelet disorder; wound;
 XX heart attack; stroke; scarring; autoimmune disorder; allergic reaction;
 XX asthma; allergic asthma; respiratory problem; anaphylaxis;
 XX hypersensitivity; blood group incompatibility; organ rejection;
 XX graft versus host disease; inflammatory condition;
 XX ischemia-reperfusion injury; endotoxin lethality; arthritis;
 XX complement-mediated hyperacute rejection; nephritis; lung injury;
 XX inflammatory bowel disease; Crohn's disease; infection.
 OS Homo sapiens.
 XX
 PN WO9935160-A1.
 XX

PD 15-JUL-1999.
 PF 06-JAN-1999; 99WO-US00120.
 XX AC AAY23885;
 PR 09-JAN-1998; 98US-0070875.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Moore PA, Ruben SM, Wei Y;
 XX WPI; 1999-430382/36.
 DR N-PSDB; AAX86148.
 XX New nucleic acids encoding human FK506 binding proteins
 PS Claim 12; Fig 4; 87pp; English.
 XX The present sequence represents a human FK506 binding protein 65
 CC (FKBP65). It is a splice variant of the sequence given in AAX86147.
 CC The polypeptide or polynucleotide may be useful in treating deficiencies
 CC or disorders of the immune system, by activating or inhibiting the
 CC proliferation, differentiation, or mobilization (chemotaxis) of immune
 CC cells. They may be useful in treating or detecting deficiencies or
 CC disorders of hematopoietic cells, to increase differentiation and
 CC proliferation of hematopoietic cells including the pluripotent stem
 CC cells, in an effort to treat those disorders associated with a decrease
 CC in certain types of hematopoietic cells. They can be used to modulate
 CC hemostatic or thrombolytic activity, e.g. an increase can treat blood
 CC coagulation disorders, blood platelet disorders or wounds resulting from
 CC trauma, surgery or other causes, or a decrease can treat heart attacks,
 CC strokes or scarring. They can also treat autoimmune disorders, allergic
 CC reactions and conditions such as asthma (particularly allergic asthma)
 CC or other respiratory problems, anaphylaxis, hypersensitivity to an
 CC antigenic molecule, or blood group incompatibility, organ rejection or
 CC graft versus host disease, inflammatory conditions, both chronic and
 CC acute, including inflammation associated with infection,
 CC ischemia-reperfusion injury, endotoxin lethality, arthritis,
 CC complement-mediated hyperacute rejection, nephritis, cytokine or
 CC chemokine induced lung injury, inflammatory bowel disease, or Crohn's
 CC disease. They can also be used to treat viral, bacterial, fungal and
 CC parasitic infections.
 XX Sequence 388 AA;
 SQ Query Match 52.6%; Score 1606; DB 20; Length 388;
 Best Local Similarity 98.1%; Pred. No. 3.8e-147;
 Matches 302; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 195 TVVGIGWLPDGMKGLLGMVCKRITITPPFLAYGEDGDKDIPQASLVDVALLDLH 254
 DB 1 TYGEIGWLPDGMKGLLGMVCKRITITPPFLAYGEDGDKDIPQASLVDVALLDLH 60
 QY 255 NPKDSISIKVVPNCERISQSGDFLTYHNGTLLDGTLPSSYRNFTFTYIGQGV 314
 DB 61 NPKDSISIKVVPNCERISQSGDFLTYHNGTLLDGTLPSSYRNFTFTYIGQGV 120
 QY 315 IPQMDGLLCVCI GERXIVPPHLYGEGRGNI PGSAVLVDI HIVDFHNPDSISIT 374
 DB 121 IPQMDGLLCVCI GERXIVPPHLYGEGRGNI PGSAVLVDI HIVDFHNPDSISIT 180
 QY 375 SHYKPPDCSVLSKKGDLKYHYNASLLDGTLDSTWNLGKTYNVLGSGQVVLGMDMGLR 434
 DB 181 SHYKPPDCSVLSKKGDLKYHYNASLLDGTLDSTWNLGKTYNVLGSGQVVLGMDMGLR 240
 QY 435 EMCVGEKRTVITPPHLYGEGAGVDGVPASVLVFDIEXLELVAGLPEGYMTFWNGVSP 494
 DB 241 EMCVGEKRTVITPPHLYGEGAGVDGVPASVLVFDIEXLELVAGLPEGYMTFWNGVSP 300
 QY 495 NLFEEIDK 502
 DB 301 NLFEEINK 308

RESULT 7
 AAY23885
 ID AAY23885 standard; Protein; 441 AA.
 AC AAY23885;
 DT 21-SEP-1999 (first entry)
 DE Amino acid sequence of a FK506 binding protein 65.
 XX Human; FK506 binding protein; FKBP65; immune system disorder;
 KW immune cell; hematopoietic cell disorder; thrombolytic activity;
 KW blood coagulation disorder; blood platelet disorder; wound;
 KW heart attack; stroke; scarring; autoimmune disorder; allergic reaction;
 KW asthma; allergic asthma; respiratory problem; anaphylaxis;
 KW hypersensitivity; blood group incompatibility; organ rejection;
 KW graft versus host disease; inflammatory condition;
 KW ischemia-reperfusion injury; endotoxin lethality; arthritis;
 KW complement-mediated hyperacute rejection; nephritis; lung injury;
 KW inflammatory bowel disease; Crohn's disease; infection.
 OS Homo sapiens.
 XX WO9935160-A1.
 XX 15-JUL-1999.
 XX 06-JAN-1999; 99WO-US00120.
 XX 09-JAN-1998; 98US-0070875.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Moore PA, Ruben SM, Wei Y;
 WPI; 1999-430382/36.
 N-PSDB; AAX86148.
 XX New nucleic acids encoding human FK506 binding proteins
 Claim 12; Fig 2; 87pp; English.
 The present sequence represents a human FK506 binding protein 65
 (FKBP65). It is a splice variant of the sequence given in AAX86145.
 The polypeptide or polynucleotide may be useful in treating deficiencies
 or disorders of the immune system, by activating or inhibiting the
 proliferation, differentiation, or mobilization (chemotaxis) of immune
 cells. They may be useful in treating or detecting deficiencies or
 disorders of hematopoietic cells, to increase differentiation and
 proliferation of hematopoietic cells including the pluripotent stem
 cells, in an effort to treat those disorders associated with a decrease
 in certain types of hematopoietic cells. They can be used to modulate
 hemostatic or thrombolytic activity, e.g. an increase can treat blood
 coagulation disorders, blood platelet disorders or wounds resulting from
 trauma, surgery or other causes, or a decrease can treat heart attacks,
 strokes or scarring. They can also treat autoimmune disorders, allergic
 reactions and conditions such as asthma (particularly allergic asthma)
 or other respiratory problems, anaphylaxis, hypersensitivity to an
 antigenic molecule, or blood group incompatibility, organ rejection or
 graft versus host disease, inflammatory conditions, both chronic and
 acute, including inflammation associated with infection,
 ischemia-reperfusion injury, endotoxin lethality, arthritis,
 complement-mediated hyperacute rejection, nephritis, cytokine or
 chemokine induced lung injury, inflammatory bowel disease, or Crohn's
 disease. They can also be used to treat viral, bacterial, fungal and
 parasitic infections.
 Sequence 441 AA;
 Query Match 45.8%; Score 1399; DB 20; Length 441;
 Best Local Similarity 58.0%; Pred. No. 6.1e-127;
 Matches 255; Conservative 77; Mismatches 102; Indels 6; Gaps 4;

134 FDVLLMDIWNSEDQVQIHTYFKPPSCPRTIQVSDFVRVHYNGTFLDGTLPDSSNNRMKY 193
Db 1 FDVLLDWNKEDTVQVSTLLRPPHPCPRMVGDFVRVHYNGTLLDGTSTFDTYSKGGTY 60
Qy 194 DTYVIGIHLIPGMDKGLLCMCVGEKRIITIPFLAYGDDGKDIPOQASLVEDVALLDL 253
Db 61 DTYVSGWLIKGMDOGLGMCGERKIIIPFLAYGKGTVPQASLVFHVLLIDV 120
Qy 254 HNPKDSISIEKNVPCNERISQSGDFTYHYNGTLLDGTLPDSSYSNRRTFTDYVIGQY 313
Db 121 HNPKDAVQLETLPPGCVRRAGAGDFVRVHYNGSLMDGTLPDSSYSNNHTVNTYVIGQY 180
Qy 314 VIPGMDGELLGVCIGKEXIIVPPHLYGEBGRN-IPGSVAVLFDIIVHIDFHPNPSDIS 372
Db 181 IIPGMDQLOGACMGERRITIPPLAYGNGTGDKIPGSVAVLIFNVHIDFHPNPDVVE 240
Qy 373 ITSHYKPPD-CSVLSKKGDKLVKHYNASLLDGTLLDSTWNLGKTYNIVLGSQVVLGMDM 431
Db 241 IRTLSPBETCNETTKLGDVFRVHYNCSLLDGTQFTSHDYCAPQEAATLGANKVIEGLDT 300
Qy 432 GLREMCVGEKRTVIIIPPHLYGEGAGVDGVPGSVAVLFDIEXLELVAGLPBGYMFVNGE 491
Db 301 GLQGMCGERRQLIIVPPHLAGESGARG-VPGSALLFEVELVSREDGLPTGYLFWHKD 359
Qy 492 VSPNLFEEIDKNGEVLLESESEYIHAQVASKGLAPGDAELIVKMMFTNDRNGDG 551
Db 360 PPNLFFEDIDLKNGEVPPEEFTFIKAQVSEKGRMLPGQPEKTIGDMFQNDNRQDG 419
Qy 552 KYTAEFKL---XDOEAKHD 568
Db 420 KITVDELKLSDEDEERVHE 432
RESULT 8
ID AAB54356
XX AAB54356 standard; Protein; 434 AA.
AC AAB54356;
XX
XX 09-MAR-2001 (first entry)
XX Human pancreatic cancer antigen protein sequence SEQ ID NO:808.
XX Human; pancreas; pancreatic cancer; pancreatic cancer antigen;
KW detection; diagnosis; identification; cytostatic; neuroprotective;
KW neurotropic; immunomodulatory; relaxant; contraceptive; gynaecological;
KW antiinflammatory; cardiac; gene therapy; chromosome mapping;
KW linkage analysis; tissue identification; tissue typing; forensic;
KW neural; immune system; muscular; reproductive; gastrointestinal;
KW pulmonary; cardiovascular; renal; proliferative.
XX
OS Homo sapiens.
XX
XX WO200055320-A1.
XX
XX 21-SEP-2000.
XX
XX 08-MAR-2000; 2000WO-US05989.
XX
XX 12-MAR-1999; 99US-0124270.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX
XX WPI; 2000-579444/54.
XX N-PSDB; AAC99121.
XX
XX New nucleic acid that is a pancreatic cancer antigen for preventing,
PT treating, or ameliorating a medical condition, particular pancreatic
PT cancer, or for use in assays for diagnosing a pathological condition -
XX
XX Claim 11; Page 1260-1261; 1379pp; English.
PS

XX AAC98773 to AAC99231 encode the human pancreatic cancer associated
CC proteins, called pancreatic cancer antigens, given in AAB54008 to
CC AAB54466. The human pancreatic cancer antigens have cytostatic,
CC neuroprotective, neurotropic, immunomodulatory, relaxant, contraceptive,
CC gynaecological, cardiac and antiinflammatory activities, and can be used
CC in gene therapy. The polynucleotide and proteins can be used for
CC preventing, treating, or ameliorating a medical condition or in assays
CC for diagnosing a pathological condition or a susceptibility to one in a
CC subject. Binding partners to the proteins and the activity of the
CC proteins can be identified. The pancreatic cancer antigens can be used to
CC detect, treat or prevent pancreatic disorders, especially cancer.
CC Agonists and antagonists to the antigens can be screened for. The
CC pancreatic cancer antigen polynucleotides can be used to design nucleic
CC acid hybridisation probes that can be used in chromosome mapping, linkage
CC and diagnostic methods. The proteins can be used to generate antibodies
CC which are used to purify, detect and target the polypeptides, including
CC both in vivo and in vitro diagnostic and therapeutic methods. The
CC proteins can be used to treat or prevent neural, immune system, muscular,
CC reproductive, gastrointestinal, pulmonary, cardiovascular, renal or
CC proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
CC sequences used in the exemplification of the present invention.
XX
SQ Sequence 434 AA;
Query Match 44.3%; Score 1354; DB 21; Length 434;
Best Local Similarity 57.5%; Pred. No. 1.4e-122;
Matches 249; Conservative 76; Mismatches 102; Indels 6; Gaps 4;
Qy 141 IWNSEDQVQIHTYFKPPSCPRTIQVSDFVRVHYNGTFLDGTLPDSSNNRMKYDTYVIG 200
Db 1 IRHEEDTVQVSTLLRPPHPCPRMVGDFVRVHYNGTLLDGTSTFDTYSKGGTYDTYVIG 60
Qy 201 WLIIPGMDKGLLCMCVGEKRIITIPPLAYGDDGKDIPOQASLVEDVALLDLHNPKDSI 260
Db 61 WLIKGMDOGLGMCGERKIIIPPLAYGKGTVPQASLVFHVLLIDVHNPDAV 120
Qy 261 STENKVPENCERISQSGDFTYHYNGTLLDGTLPDSSYSNRRTFTDYVIGQYVIPGMD 320
Db 121 QLETLPPGCVRRAGAGDFVRVHYNGSLMDGTLPDSSYSNRHTYNTYVIGQYIIPGMDQ 180
Qy 321 GLLGVICIGKRXIIVPPHLYGEBGRN-IPGSVAVLFDIIVHIDFHPNPSDISITSHYP 379
Db 181 GLQACMGERRITIPPLAYGNGTGDKIPGSVAVLIFNVHIDFHPNPDVVEIRLSRP 240
Qy 380 PD-CSVLSKKGDKLVKHYNASLLDGTLLDSTWNLGKTYNIVLGSQVVLGMDGLREMCV 438
Db 241 SETCNETTKLGDVFRVHYNCSLLDGTQFTSHDYCAPQEAATLGANKVIEGLDTLQGM 300
Qy 439 GEKRTVIIIPPHLYGEGAGVDGVPGSVAVLFDIEXLELVAGLPBGYMFVNGEVSPLFE 498
Db 301 GERQLIIVPPHLAGESGARG-VPGSALLFEVELVSREDGLPTGYLFWHKDPPANLFE 359
Qy 499 EIDKNGEVLLESESEYIHAQVASKGLAPGDAELIVKMMFTNDRNGDGKVTAEF 558
Db 360 DMDLNDKNGEVPPEEFTFIKAQVSEKGRMLPGQPEKTIGDMFQNDNRQDGKITVDEL 419
Qy 559 KL---XDOEAKHD 568
Db 420 KLSDEDEERVHE 432
RESULT 9
ID AAB41125
XX AAB41125 standard; Protein; 166 AA.
AC AAB41125;
XX
XX 23-AUG-2002 (first entry)
XX Human ovarian antigen HOFMO23, SEQ ID NO:2257.
XX
XX

Sequence 1241 AA;

Query Match 24.9%; Score 760; DB 22; Length 1241;
Best Local Similarity 39.4%; Pred. No. 4e-64;
Matches 175; Conservative 62; Mismatches 117; Indels 90; Gaps 12;

QY 201 WLI-PQMDKGLLCVCGEKKRIITIPFLAYGEGDGKD-----237
DB 6 WLADQGHGGAAGHVSWEKEIIIPFLAYGEGYGEKGKHKGFRRRGKQASTYSCS 65
QY 238 -----IPQASLVFVALLDHNPKDSISIEKVVPCERISQSGDPL 281
DB 66 GCILHEGIOPRTQGTIVPQASLVFVALLDHNPKDAVQLETLELPCCVRRAGADPM 125
QY 282 TYHNGTLDTGLTSSYSRNRFTYIGQYVPGMDGLLQVCIQGEKXIVVPHLY 341
DB 126 RYHNGSLMDGTLTSSYSRNRFTYIGQYVPGMDGLLQVCIQGEKXIVVPHLY 185
QY 342 GREGGN-IPGSAVLVFDTHVDFHNPDSISITSHYKPPD-CSVLKKGDKYLVKHYNAS 399
DB 186 GENGTDKIPGSAVLVFNHVDHNPADVEIRTSRSEYCNCTKGLGDFVRYHNC 245
QY 400 LLDGTLDDSTWNLGKTYNVLGSGQVVLGMDGLREMCVGEKRTVIIPHLGYGEAGVDG 459
DB 246 LLDGTLFTSHDYGAQETAGANKVIEGLDTGLQCMCVGERQLIVPPLAHGESG--G 303
QY 460 EYVGSVAVFDIEXLEL-----VAGLPGYME-----IWN-- 489
DB 304 VTKIVSVLKYLYAYELHPCIQKRWWEKIPLAKTTLEKTWLPHEIGRCVYLELDQAWAQ 363
QY 490 --GEVSNLPFE--IDKQNGBVLL---EEFSYIHAQVASKGKLAQPGDAELIVKXN 541
DB 364 NYGEKQOQCAEBEGDIEWQLNASVLVAQAEASLYEDRIITREKDMRVEDEPEKVKQW 423
QY 542 FTNQDRNGDKVTAEBFKLXQEA 565
DB 424 ----DHSEDEKETDE-----DDEA 438

RESULT 11
AA57114
ID AA57114 standard; Protein; 366 AA.
XX
AC AA57114;
XX
DT 13-MAR-2001 (first entry)
XX
DE Human prostate cancer antigen protein sequence SEQ ID NO:1692.
XX
KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
KW vulnary; gastrointestinal; nephrotropic; antiinfective; gynaecological;
KW antibacterial; gene therapy; neural; immune; reproductive; renal;
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KW wound; infectious disease.
XX
OS Homo sapiens.
XX
PN W0200055174-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US05988.
XX
PR 12-MAR-1999; 99US-0124270.
XX
PA (HOMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-587513/55.
XX
DR N-PSDB; AAF16317.
XX
PT Prostate cancer associated gene sequences, referred to as prostate

cancer antigens, useful for treatment, prevention, and diagnosis of
disorders such as prostate cancer -
XX
PS Claim 11; Page 2162-2164; 2338pp; English.
XX
CC AAF15566 to AAF16505 encode the human prostate cancer associated
CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
CC The prostate cancer antigens can have neuroprotective, cytostatic,
CC cardioactive, immunomodulatory, muscular, vulnary, gastrointestinal,
CC nephrotropic, antiinfective, gynaecological and antibacterial activities,
CC and can be used in gene therapy. The prostate cancer antigen
CC polynucleotides may be used for detection of prostate cancer, chromosome
CC identification, as chromosome markers, and for numerous other diagnostic
CC or research purposes. The prostate cancer antigens may be used to treat
CC disorders such as neural, immune, muscular, reproductive
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
CC AAB57303 represent sequences used in the exemplification of the present
XX invention.

XX SQ Sequence 366 AA;
Query Match 24.3%; Score 743; DB 21; Length 366;
Best Local Similarity 43.5%; Pred. No. 2.6e-63;
Matches 165; Conservative 45; Mismatches 91; Indels 78; Gaps 10;

QY 6 WRPP-----PP-----PLLLLLWVT-----GQAPVAGLGD 33
DB 20 WRLPRSPSPAVPTPTMPFAGPPSHSLRLQLLLVQAVGRLGRASPAGPLED 79
QY 34 AELQIERRFVDPBCPTVRSGDFVRYHYVGTTPDGQKFDSSYDRDSTFNVFGKGLITG 93
DB 80 --VVIERYHIPRACPREVQMGDFVRYHNGTFEDGKFDSSYDRNTLVAIVVGVRLITG 137
QY 94 MDQALVGMCMVNERFVKIPKLAIGNERVSQVTPNSVLHFDVLLMDINSEDOVQIHTY 153
DB 138 MDRGLMGCMVNERRLIVPPLHLYGSGTLAGLIPDPATLYFDVLLDWNKEDTVQVSTL 197
QY 154 FKPPSCPTTIQVDFVRYHYNGTFLDGLTLPDSSHNRMKTYDVTYVIGLWLPMDKGLGM 213
DB 198 LRPPHCFPMVQDGFVRYHYNGTLLDGTSTFSTYSKGTIYDVTYVGSWLLKMGMDQGLGM 257
QY 214 CVGEKRIITIPFLAYGEGDGKDIPQASLVFVALLDLH-----NPKDSISIE 264
DB 258 CPGERKKIIPFLAYGEGYGE--GQG-----HKGFRRRGKQASTYSCSG 304
QY 265 KVPENCERISQSGDFLYHYNGTLLDGTFLDSSYSRNRFTDYIGQY----VIPGMD 320
DB 305 CILHEGIQPTQGG-----MKSTL-----GATKKGCFGRWWLTLVIPALWE 346
QY 321 GLLGVCIQGEKXIVVPPHL 339
DB 347 AKAGSGRQGIETTVKPL 365

RESULT 12
AA573884
ID AA573884 standard; Protein; 316 AA.
XX
AC AA573884;
XX
DT 21-SEP-1999 (first entry)
XX
DE Amino acid sequence of FK506 binding protein 65 (FKBP65).
XX
KW Human; FK506 binding protein; FKBP65; immune system disorder;
KW immune cell; hematopoietic cell disorder; thrombolytic activity;
KW blood coagulation disorder; blood platelet disorder; wound;
KW heart attack; stroke; scarring; autoimmune disorder; allergic reaction;
KW asthma; allergic asthma; respiratory problem; anaphylaxis;
KW hypersensitivity; blood group incompatibility; organ rejection;
KW graft versus host disease; inflammatory condition;
KW ischemia-reperfusion injury; endotoxin lethality; arthritis;

RESULT 14
AB64697
ID AB64697 standard; Protein; 216 AA.
XX
AC AB64697;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 20883.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
WI; 2001-656860/75.
DR N-PSDB; ABL08800.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signalling and cell-cell
interactions -
XX
PS Disclosure; SEQ ID NO 20883; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
capable of detecting 1000 or more genes from Drosophila. The invention is
useful in developmental biology and in elucidating cell signalling and
cell-cell interactions in higher eukaryotes for the development of
insecticides, therapeutics and pharmaceutical drugs. The invention
discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
sequences (ABL01840-ABL16175) and the encoded proteins
(AB857737-AB872072).
CC The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 216 AA;
Query Match 10.1%; Score 309; DB 22; Length 216;
Best Local Similarity 23.8%; Pred. No. 1.8e-21;
Matches 83; Conservative 50; Mismatches 58; Indels 158; Gaps 8;
QY 241 QASLVPFVALDLHNPXDSISIKV-----PENCERISQSGDFLTYHNGT 288
DB 3 KSNLVISCLLL-----VAISNSLRAQDLKVEVISTPEVCQKSKGDSLFTHVGT 54
QY 289 L-LDGTLPDSSYSNRRTFDYVIGQYVPGMDGLGVCIGEKRXIVVPPHLYGGEGRG 347
DB 55 LQADKKFDSFDPQFTQLGAGQVIGWDQQLNMCVGEKRLIIPQLGYDQAG 114
QY 348 NPGSAVLVFDIHDVFNHPSDSISITSHYKPPDCSVLSKKGDYLYKHYNASLLDGLLD 407
DB 115 NV----- 116
QY 408 STWNLKTYNIVLGGQVVLGMDMLREMCVGEKRTVIIPHLGYGEAGVDGVPGSVIL 467
DB 117 -----IppKATL 123
QY 468 VFDIEXLELVAGLPEGYFIWNGEVSPLNLFEDKDGNGEVLLEFSEYIHAQVASKGK 527

Db 124 LFDVELIN-----IGNAPTTNVFKEIDNADKQLSREVSEYLLKKQMTAVEGQ 172
QY 528 -----LAFGFDALIVKXMTNQDRNGDGKVTAEFFKLXQDAKHD 568
DB 173 DSEELKNMLA---ENDKLVEEIFQHEDKXNGFTSHDEF-----SGPKHD 214
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AAU87239
ID AAU87239 standard; Protein; 131 AA.
XX
AC AAU87239;
XX
DT 05-JUN-2002 (first entry)
XX
DE Novel central nervous system protein #149.
XX
KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
KW adenocarcinoma; reproductive system disorder; testicular feminisation;
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
KW respiratory disorder; renal disorder; kidney failure; blood disorder;
KW myocardial infarction; wound healing; cell proliferation; skin aging;
KW food additive; food preservative; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200155318-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01332.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0217496.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.


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QY 506 GEVLLEEFSEYIHAQVASKGKGLAPGFDALFVKNMFTNQDRNGDGKVTABEFKL---XD 562
Db 64 GEVPPPEEFSTFIKAQVSEKGRLMFGQDPEKTIGDMFQONQDRNQDGKITVDELKLSDED 123
QY 563 QEAKHD 568
Db 124 EERVHE 129
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Search completed: April 26, 2003, 06:53:05
Job time : 42.2691 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 26, 2003, 06:48:54 ; Search time 14.5233 Seconds
(without alignments)
1162.874 Million cell updates/sec

Title: US-09-225-502-6
Perfect score: 3054
Sequence: 1 MAFKWRPPPPPLLLLLLV.....AEEFKLXDQAKHVDVTLNLA 574

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/5B-COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1750.5	57.3	581	2	US-08-989-386-7
2	1742	57.0	582	2	US-08-989-386-1
3	244.5	8.0	135	1	US-08-336-618-20
4	242.5	7.9	141	1	US-07-822-966B-6
5	242.5	7.9	142	1	US-08-336-618-18
6	242.5	7.9	142	5	PCT-US92-03993-7
7	231.5	7.6	141	2	US-08-803-899-6
8	230.5	7.5	107	3	US-08-894-173-69
9	230.5	7.5	107	3	US-08-894-173-83
10	230.5	7.5	107	4	US-09-398-193-69
11	230.5	7.5	107	4	US-09-398-193-83
12	230.5	7.5	119	5	PCT-US92-03993-1
13	230.5	7.5	120	1	US-08-336-618-17
14	230	7.5	104	3	US-08-894-173-86
15	230	7.5	104	4	US-09-398-193-86
16	228	7.5	458	1	US-08-336-618-24
17	228	7.5	459	1	US-08-336-618-12
18	228	7.5	459	1	US-08-336-618-26
19	227.5	7.4	105	3	US-08-894-173-84
20	227.5	7.4	105	4	US-09-398-193-84
21	213	7.0	99	5	PCT-US92-03993-5
22	207	6.8	107	3	US-08-894-173-66
23	207	6.8	107	3	US-08-894-173-79
24	207	6.8	107	4	US-09-398-193-66
25	207	6.8	107	4	US-09-398-193-79
26	207	6.8	113	5	PCT-US92-03993-4
27	207	6.8	114	1	US-08-336-618-16

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Sequence 4, Appli
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Sequence 15, Appli
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Sequence 4, Appli
Sequence 22, Appli
Sequence 13, Appli
Sequence 1, Appli
Sequence 7, Appli
Sequence 67, Appli

ALIGNMENTS

RESULT 1
US-08-989-386-7
; Sequence 7, Application US/08989386
; Patent No. 5989860
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN ISOMERASE HOMOLOGS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,386
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0443 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; LENGTH: 581 amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 894162
; US-08-989-386-7

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0443 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 582 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: OVARUT01
; CLONE: 2255114
; US-08-989-386-1

Query Match          57.0%; Score 1742; DB 2; Length 582;
Best Local Similarity 56.4%; Pred. No. 1.2e-166;
Matches 326; Conservative 99; Mismatches 131; Indels 22; Gaps

QY 10 PP-----PLLLLLLWVT-----GQAAPVAGLGSDAELOIERFFVDPDECPTRVRSGD 55
Db 6 PPSHSLLRLPLQLLLLLVVQAVGRGLGRASPAGGPLED--VVIERYHIPRACPREVQMGD 63
QY 56 FVRHYHVGTFPDGQKFDSSYDRDSTFNFVVGKGQLITGMDQALGMCVNERRFVKIPPKL 115
Db 64 FVRYHYNGTFECKKFDSSYDRNTLVAIVVGVGRLLITGMDRGLGMCVNERRLLVPPHL 123
QY 116 AYGNERSVGVPPNSVLHFDVLLMDIWNSEDQVHTYFKPPSCPTTIQVSDFVRYHYNG 175
Db 124 GYGSISGLAGLIPDATALPYDVLVDVNNKEDTVQVSTLLRPCHPCRMVQDGFVRYHYNG 183
QY 176 TFLDGTFLPDSHNRKMTYDTYVIGIWLIPGMDKGLLGCMVGKRIITIPFLAYGEDGDG 235
Db 184 TLLDGTSPDTSYSGKGYDTYVYVSGWLLKGMDOGLLGMCPGBRXXIIPFLAYGEKGYG 243
QY 236 KDIPQASLVFDVALLDHNPKDSISIKNVVPENCERISQSGDFTLTHYNGTLLDGTULF 295
Db 244 TVIPFQASLVFVLLIDVHNPKDAVQLETLPPGCVRRAGAGDFMYHYNGSLMDGTFL 303
QY 296 DSSYSRNRFTDYIGQYVYVPGMDGGLLGVCIGKRXIIVPHLGVBEGRN-IPGSVAV 354
Db 304 DSSYSRNYTYIIGQYIIPGMDQGLQACNGERRITIPHLAYGENTGDKIPGSVAV 363
QY 355 LVFDIIVIDFHNPPSSISITSHYKPPD-CSVLKSGDYLYKHYNASLLDGTLLDSTWNLG 413
Db 364 LIFNVHVIDFHNPAVDVEIRTLRSRSETCNETTKLGDVFRHYNGSLDGTQLFTSHDYG 423
QY 414 KTYNTVLGSGQVVLGMDGLRMCVGEKRTVIIPPHLGVEAGVDEVPGSVAVLVDIEKX 473
Db 424 APOEATLGANKVIEGLDTGLQGCVCGERQLIVPHLAHGESGARG-VPGSAVLLFEVL 482
QY 474 LELVAGLPGCYWFIWNGEVSVPNLFFBEIDKDGNGEVLLEBFPSYIHAQVASHGKGLAPGD 533
Db 483 VSREPDGLFTGYLVFVHKDPANLFFDMDLNDKGDVPPPEFSTFIKAQVSEGGRLMPGOD 542
QY 534 ASLIVKNNFTNQRNDGDKGVTAEFKL---XDQEAARD 568
Db 543 PEKTIQDMFQNDNRQDQKTIIVDELKLLKSDSEDEERVHE 580

RESULT 3
US-08-336-618-20
; Sequence 20, Application US/08336618
; Patent No. 5763590
; GENERAL INFORMATION:
; APPLICANT: Peattie, Debra A.

```

;; APPLICANT: Harding, Matthew W.
;; APPLICANT: Livingston, David J.
;; TITLE OF INVENTION: ISOLATION OF AN MR 52,000 FK506 BINDING
;; TITLE OF INVENTION: PROTEIN AND MOLECULAR CLONING OF A CORRESPONDING HUMAN
;; TITLE OF INVENTION: CDNA
;; NUMBER OF SEQUENCES: 32
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Hamilton, Brook, Smith and Reynolds, P.C.
;; STREET: Two Militia Drive
;; CITY: Lexington
;; STATE: Massachusetts
;; COUNTRY: U.S.A.
;; ZIP: 02173
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/336,618
;; FILING DATE: 09-NOV-1994
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/963,325
;; FILING DATE: 16-OCT-1992
;; APPLICATION NUMBER: US 07/777,752
;; FILING DATE: 11-OCT-1991
;; PRIOR APPLICATION DATA: PCT/
;; APPLICATION NUMBER: PCT/
;; FILING DATE: 09-OCT-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Granahan, Patricia
;; REGISTRATION NUMBER: 32,227
;; REFERENCE/DOCKET NUMBER: VP191-06A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-861-9240
;; TELEFAX: 617-861-9540
;; INFORMATION FOR SEQ ID NO: 20:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 135 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-336-618-20

Query Match 8.0%; Score 244.5; DB 1; Length 135;
Best Local Similarity 43.3%; Pred. No. 7.4e-17;
Matches 55; Conservative 21; Mismatches 50; Indels 1; Gaps 1;
QY 16 LLLWVTGQAPVAGLSGDAELQIERRFVDPDCPRTVRSRQDFVRHYVGT-FPDGQKPDSS 74
DB 5 IYLFVTFSTILAGSLSDLEIGIKRIPVEDCLIKAMPDGVKHYTGSLLESQTVFSS 64
QY 75 YDRSTFNVFVGKQLITGMDQALVGMVNRFRFKIPPKLAYGNRVSGVIPPNSVLHF 134
DB 65 YSRGSPAFELGVRVIGKWDQGVAGMVGKRLQIPSSLAYGRGVGVIPPSADLVF 124
QY 135 DVLMDI 141
DB 125 DVELVDV 131

RESULT 4
US-07-822-966B-6
; Sequence 6, Application US/07822966B
; Patent No. 5498597
; GENERAL INFORMATION:
; APPLICANT: Steven J. Burakoff
; APPLICANT: Stuart L. Schreiber
; APPLICANT: Barbara E. Bierer
; TITLE OF INVENTION: FKBP-13, AN FK506-BINDING
; TITLE OF INVENTION: IMMUNOPHILIN
; NUMBER OF SEQUENCES: 6

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Richardson P.C.
;; STREET: 225 Franklin Street
;; CITY: Boston
;; STATE: Massachusetts
;; COUNTRY: U.S.A.
;; ZIP: 02110-2804
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; COMPUTER: IBM PS/2 Model 502 or 555X
;; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
;; SOFTWARE: WordPerfect (Version 5.0)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/822,966B
;; FILING DATE: January 17, 1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fraser, Janis K.
;; REGISTRATION NUMBER: 34,819
;; REFERENCE/DOCKET NUMBER: 00530/052001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 542-5070
;; TELEFAX: (617) 542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 141 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-07-822-966B-6

Query Match 7.9%; Score 242.5; DB 1; Length 141;
Best Local Similarity 47.7%; Pred. No. 1.3e-16;
Matches 51; Conservative 17; Mismatches 36; Indels 3; Gaps 2;
QY 257 KDSISIKNVKVPENCERISQSGDFLTYYHNGTLLDGTFLDSSYSRNRFTDTYIGQGVIP 316
DB 29 KLIQGVKKRV--DHCPIKSRKGDVLMHYTKLEDCTEDFSSLPQNPQPFVFSIGTGQVIK 86
QY 317 GMDEGLLVGICGKRXIVVPHLGYGEGR-GNIPGSAVLVFDIHWI 362
DB 87 GWDQGLLGWCEGKRLVPSLGYGEGRAPPKIPGATLVFEVELL 133

RESULT 5
US-08-336-618-18
; Sequence 18, Application US/08336618
; Patent No. 5763590
; GENERAL INFORMATION:
; APPLICANT: Peattie, Debra A.
; APPLICANT: Harding, Matthew W.
; APPLICANT: Livingston, David J.
; TITLE OF INVENTION: ISOLATION OF AN MR 52,000 FK506 BINDING
; TITLE OF INVENTION: PROTEIN AND MOLECULAR CLONING OF A CORRESPONDING HUMAN
; TITLE OF INVENTION: CDNA
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith and Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,618
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 435

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/963,325
; FILING DATE: 16-OCT-1992
; APPLICATION NUMBER: US 07/777,752
; FILING DATE: 11-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/
; FILING DATE: 09-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: VP191-06A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 142 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-336-618-18

Query Match      7.9%; Score 242.5; DB 1; Length 142;
Best Local Similarity 47.7%; Pred. No. 1.3e-16;
Matches 51; Conservative 17; Mismatches 36; Indels 3; Gaps 2;

QY 257 KDSISIEKVVPCERISQSGDLTYHYNGTLLDGTLLFDSSYSRNRFTDTYIGQGVIP 316
Db 30 KLIQGVKRV--DHCPIKSRKGDVLMHMTYTKLEGTEDFSSLPQNPQPFVSLGTGVK 87
QY 317 GMDGGLGVCIGEKRXIVVPHLGYGEGR-GNIPGSAVLVFDIHI 362
Db 88 GWDQGLGMCGEKRLVIPSELGYGERGAPPKIPGGATLVFEVLL 134

RESULT 6
PCT-US92-03993-7
; Sequence 7, Application PC/TUS9203993
; GENERAL INFORMATION:
; APPLICANT: Harding, Matthew W.
; TITLE OF INVENTION: RFKBP: A NOVEL PROLYL ISOMERASE AND
; TITLE OF INVENTION: RAPAMYCIN/FK506 BINDING PROTEIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/03993
; FILING DATE: 19920507
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/697,113
; FILING DATE: 08-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: VP191-05A PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 142 amino acids

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; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US92-03993-7

Query Match      7.9%; Score 242.5; DB 5; Length 142;
Best Local Similarity 47.7%; Pred. No. 1.3e-16;
Matches 51; Conservative 17; Mismatches 36; Indels 3; Gaps 2;

QY 257 KDSISIEKVVPCERISQSGDLTYHYNGTLLDGTLLFDSSYSRNRFTDTYIGQGVIP 316
Db 30 KLIQGVKRV--DHCPIKSRKGDVLMHMTYTKLEGTEDFSSLPQNPQPFVSLGTGVK 87
QY 317 GMDGGLGVCIGEKRXIVVPHLGYGEGR-GNIPGSAVLVFDIHI 362
Db 88 GWDQGLGMCGEKRLVIPSELGYGERGAPPKIPGGATLVFEVLL 134

RESULT 7
US-08-803-899-6
; Sequence 6, Application US/08803899
; Patent No. 5912224
; GENERAL INFORMATION:
; APPLICANT: DONAHOE, PATRICIA K.
; APPLICANT: WANG, TONGWEN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ENHANCING
; TITLE OF INVENTION: CELLULAR RESPONSE TO TGF-BETA LIGANDS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/803,899
; FILING DATE: 02/21/1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/012,054
; FILING DATE: 02/22/1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 0609,4240001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 141 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-803-899-6

Query Match      7.8%; Score 231.5; DB 2; Length 141;
Best Local Similarity 46.7%; Pred. No. 1.6e-15;
Matches 50; Conservative 17; Mismatches 37; Indels 3; Gaps 2;

QY 257 KDSISIEKVVPCERISQSGDLTYHYNGTLLDGTLLFDSSYSRNRFTDTYIGQGVIP 316
Db 29 KLIQGVKRV--DHCPIKSRKGDVLMHMTYTKLEGTEDFSSLPQNPQPFVSLGTGVK 86
QY 317 GMDGGLGVCIGEKRXIVVPHLGYGEGR-GNIPGSAVLVFDIHI 362

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/03993
FILING DATE: 19920507
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/697,113
FILING DATE: 08-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: VP191-05A PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-03993-1

Query Match 7.5%; Score 230.5; DB 5; Length 119;
Best Local Similarity 45.0%; Pred. No. 1.6e-15;
Matches 50; Conservative 14; Mismatches 42; Indels 5; Gaps 1;

Qy 31 GSDAELQIERRFVDPDECPRTVRSQDFVRYHYVGTTPDQKFDSSYDRDSTFNVVGKQL 90
Db 7 GLQIEVQOE-----GQGTRETRRGDNVDVHYKGVLTSGKFDASYDRGEPLNFTVGQGV 61
Qy 91 ITGMDQALVGMVNERFVKIPPKLAYGNERSVGVIPNSVLHFDVLLMDI 141
Db 62 IKGWDEGLGKIGKERRKLTIAPLAYGNRAVGGIIPANSTLIFETELVGI 112

RESULT 13
US-08-336-618-17
Sequence 17, Application US/08336618
Patent No. 5763590
GENERAL INFORMATION:
APPLICANT: Peattie, Debra A.
APPLICANT: Harding, Matthew W.
APPLICANT: Livingston, David J.
TITLE OF INVENTION: ISOLATION OF AN MR 52,000 FK506 BINDING
TITLE OF INVENTION: PROTEIN AND MOLECULAR CLONING OF A CORRESPONDING HUMAN
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESSES:
ADDRESS: Hamilton, Brook, Smith and Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,618
FILING DATE: 09-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/963,325
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/777,752
FILING DATE: 11-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 09-OCT-1992

ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: VP191-06A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-618-17

Query Match 7.5%; Score 230.5; DB 1; Length 120;
Best Local Similarity 45.0%; Pred. No. 1.6e-15;
Matches 50; Conservative 14; Mismatches 42; Indels 5; Gaps 1;

Qy 31 GSDAELQIERRFVDPDECPRTVRSQDFVRYHYVGTTPDQKFDSSYDRDSTFNVVGKQL 90
Db 8 GLQIEVQOE-----GQGTRETRRGDNVDVHYKGVLTSGKFDASYDRGEPLNFTVGQGV 62
Qy 91 ITGMDQALVGMVNERFVKIPPKLAYGNERSVGVIPNSVLHFDVLLMDI 141
Db 63 IKGWDEGLGKIGKERRKLTIAPLAYGNRAVGGIIPANSTLIFETELVGI 113

RESULT 14
US-08-894-173-86
Sequence 86, Application US/08894173A
Patent No. 6090612
GENERAL INFORMATION:
APPLICANT: Medical Research Council
TITLE OF INVENTION: Adenylate cyclase and uses therefor
FILE REFERENCE: P14716C
CURRENT APPLICATION NUMBER: US/08/894,173A
CURRENT FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 86
LENGTH: 104
TYPE: PRT
ORGANISM: Yeast
US-08-894-173-86

Query Match 7.5%; Score 230; DB 3; Length 104;
Best Local Similarity 46.9%; Pred. No. 1.4e-15;
Matches 45; Conservative 16; Mismatches 35; Indels 0; Gaps 0;

Qy 381 DCSVLKKGDKYLVKHYNASLDDGTLDDSTWNLGKTYNTVLGSGQVVLGMDGLREMCVGE 440
Db 8 DCLIKAMPGDKVKVHYTGSLESTGVFDSSYSRSGPIAELGVGRVKGWDQGVAGMCVGE 67
Qy 441 KRTVIIPHLGYGAGVDGVEPGSAVLVFDIEXLEL 476
Db 68 KRLQIFSSLAYGERGVGVIPPSADLVDFDELVDV 103

RESULT 15
US-09-398-193-86
Sequence 86, Application US/09398193
Patent No. 6197581
GENERAL INFORMATION:
APPLICANT: Medical Research Council
TITLE OF INVENTION: Adenylate cyclase and uses therefor
FILE REFERENCE: P24360-
CURRENT APPLICATION NUMBER: US/09/398,193
CURRENT FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 86
LENGTH: 104

; TYPE: PRT
; ORGANISM: Yeast
US-09-398-193-86

Query Match 7.5%; Score 230; DB 4; Length 104;
Best Local Similarity 46.9%; Pred. No. 1.4e-15;
Matches 45; Conservative 16; Mismatches 35; Indels 0; Gaps 0;
Qy 381 DCSVLSKKGDYLVKHYNASLLDGTLLDSTWNLGKTYNIVLGSGGVVLGMDMGLREMCVGE 440
Db 8 DCLIKAMFGDKVKVHYTGSLESGTVFDSYSRGSPIAFELGVGRVKGWDQGVAGMCVGE 67
Qy 441 KRTVIIPPHLGYGEAGVDGEVPGSAVLVFDIEXLEL 476
Db 68 KRKLQIPSSLAYGERGVPGVIPPSSADLVFDVELVDV 103

Search completed: April 26, 2003, 06:49:51
Job time : 15.7733 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 26, 2003, 06:51:02 ; Search time 18.1541 Seconds
(without alignments)
2533.559 Million cell updates/sec

Title: US-09-225-502-6

Perfect score: 3054

Sequence: 1 MAFRGMWRPPPPPLLLLLLWV.....AEEFKLXQBAKHQDVTNLNA 574

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 301932 seqs, 80129803 residues

Total number of hits satisfying chosen parameters: 301932

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep.*
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- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW PUB.pep.*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3048	99.8	574	US-09-225-502-6	Sequence 6, Appli
2	1606	52.6	388	US-09-225-502-8	Sequence 8, Appli
3	1399	45.8	441	US-09-225-502-4	Sequence 4, Appli
4	1354	44.3	434	US-09-925-297-808	Sequence 808, App
5	743	24.3	366	US-09-925-300-1692	Sequence 1692, App
6	737	24.1	336	US-09-225-502-2	Sequence 2, Appli
7	268	8.8	222	US-10-006-856A-180	Sequence 180, App
8	268	8.8	222	US-10-006-818A-180	Sequence 180, App
9	268	8.8	222	US-10-015-393A-180	Sequence 180, App
10	268	8.8	222	US-09-946-374-180	Sequence 180, App
11	268	8.8	222	US-10-012-121A-180	Sequence 180, App
12	268	8.8	222	US-10-015-869A-180	Sequence 180, App
13	256	8.4	211	US-09-978-295A-145	Sequence 145, App
14	256	8.4	211	US-09-978-697-145	Sequence 145, App
15	256	8.4	211	US-09-978-192A-145	Sequence 145, App
16	256	8.4	211	US-09-999-832A-145	Sequence 145, App
17	256	8.4	211	US-10-001-054-4	Sequence 4, Appli
18	256	8.4	211	US-09-978-189-145	Sequence 145, App
19	256	8.4	211	US-10-028-072-384	Sequence 384, App

20	256	8.4	211	9	US-10-121-049-384	Sequence 384, App
21	256	8.4	211	9	US-10-123-904-384	Sequence 384, App
22	256	8.4	211	9	US-10-140-470-384	Sequence 384, App
23	256	8.4	211	9	US-10-175-746-384	Sequence 384, App
24	256	8.4	211	9	US-10-176-918-384	Sequence 384, App
25	256	8.4	211	9	US-10-176-921-384	Sequence 384, App
26	256	8.4	211	9	US-10-137-865-384	Sequence 384, App
27	256	8.4	211	9	US-10-140-474-384	Sequence 384, App
28	256	8.4	211	9	US-10-142-431-384	Sequence 384, App
29	256	8.4	211	9	US-10-143-114-384	Sequence 384, App
30	256	8.4	211	9	US-10-140-002-384	Sequence 384, App
31	256	8.4	211	9	US-09-978-608A-145	Sequence 145, App
32	256	8.4	211	9	US-10-142-419-384	Sequence 384, App
33	256	8.4	211	9	US-09-976-724A-189	Sequence 189, App
34	256	8.4	211	9	US-09-978-191A-145	Sequence 145, App
35	256	8.4	211	9	US-09-978-403A-145	Sequence 145, App
36	256	8.4	211	9	US-09-978-564A-145	Sequence 145, App
37	256	8.4	211	9	US-09-978-585A-145	Sequence 145, App
38	256	8.4	211	9	US-10-017-081A-145	Sequence 145, App
39	256	8.4	211	9	US-10-123-262-384	Sequence 384, App
40	256	8.4	211	9	US-10-142-423-384	Sequence 384, App
41	256	8.4	211	9	US-09-978-824-145	Sequence 145, App
42	256	8.4	211	9	US-09-981-915A-145	Sequence 145, App
43	256	8.4	211	9	US-09-999-833A-145	Sequence 145, App
44	256	8.4	211	9	US-10-121-050-384	Sequence 384, App
45	256	8.4	211	9	US-10-141-755-384	Sequence 384, App

ALIGNMENTS

RESULT 1

US-09-225-502-6

; Sequence 6, Application US/09225502A

; Patent No. US20020137127A1

; GENERAL INFORMATION:

; APPLICANT: Moore et al.

; TITLE OF INVENTION: Human FK506 Binding Proteins

; FILE REFERENCE: PF392

; CURRENT APPLICATION NUMBER: US/09/225,502A

; CURRENT FILING DATE: 1999-01-06

; PRIOR APPLICATION NUMBER: 60/070,875

; PRIOR FILING DATE: 1998-01-09

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 6

; LENGTH: 574

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-225-502-6

Query Match 99.8%; Score 3048; DB 10; Length 574;
Best Local Similarity 100.0%; Pred. No. 4.4e-259;
Matches 574; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MAFRGMWRPPPPPLLLLLLWVGTQAA	PVAGLGSDAELQIERRFVPDPCRTVRS	GDFVRYH 60
Db	1	MAFRGMWRPPPPPLLLLLLWVGTQAA	PVAGLGSDAELQIERRFVPDPCRTVRS	GDFVRYH 60
QY	61	YVGTFFDQKFDSSYDRDSTFN	VFGKQLITGMDQALVGMVNERFVKIP	PKLAYGNE 120
Db	61	YVGTFFDQKFDSSYDRDSTFN	VFGKQLITGMDQALVGMVNERFVKIP	PKLAYGNE 120
QY	121	RVSQVIPPNSVLPHFDVLLMDI	WNSEDQVQIHTYFKPSPCRPTIQVSD	FVRYHNGTFLDG 180
Db	121	RVSQVIPPNSVLPHFDVLLMDI	WNSEDQVQIHTYFKPSPCRPTIQVSD	FVRYHNGTFLDG 180
QY	181	TLFDSSHNRMKTYTYVIGI	WLIIPGMDKLLGMCVGEKRIITIP	PFPLAYGEDGDKDIPG 240
Db	181	TLFDSSHNRMKTYTYVIGI	WLIIPGMDKLLGMCVGEKRIITIP	PFPLAYGEDGDKDIPG 240
QY	241	QASLAFEDVALLDHNPKD	STSIENKVPENCERISQSGDFTYH	YNGTFLDGTFLDSSYS 300
Db	241	QASLAFEDVALLDHNPKD	STSIENKVPENCERISQSGDFTYH	YNGTFLDGTFLDSSYS 300

Db 241 QASLVFDVALLDHNPKDSISIKNVVPCNCERISQSGDLTYHYNGTLLDGLTLPDSSYS 300
Qy 301 RNRTEFTYIGQGVVPGMDGGLGVCIGKRXIVPPHLYGEGRGNTIPGSAVLVFDIH 360
Db 301 RNRTEFTYIGQGVVPGMDGGLGVCIGKRXIVPPHLYGEGRGNTIPGSAVLVFDIH 360
Qy 361 VIDFNPSDSISITSHYKPPDCSVLSKGGDKYKHYNASLLDGLTLDSTWNLGKTYNVL 420
Db 361 VIDFNPSDSISITSHYKPPDCSVLSKGGDKYKHYNASLLDGLTLDSTWNLGKTYNVL 420
Qy 421 GSGQVVLGMDGLREMCVGEKRTVIIPPHLYGEGAGVDGPGSAVLVFDIEXLELVAGL 480
Db 421 GSGQVVLGMDGLREMCVGEKRTVIIPPHLYGEGAGVDGPGSAVLVFDIEXLELVAGL 480
Qy 481 PEGYMFIMNGEVPNLFEEIDKNGEVLLEFSEYIHAQVAGSKGLAPGDAELIVN 540
Db 481 PEGYMFIMNGEVPNLFEEIDKNGEVLLEFSEYIHAQVAGSKGLAPGDAELIVN 540
Qy 541 MFTNQRNGDGKVTABEFKLDQEAHVDVTLNLA 574
Db 541 MFTNQRNGDGKVTABEFKLDQEAHVDVTLNLA 574

RESULT 2

US-09-225-502-8
; Sequence 8, Application US/09225502A
; Patent No. US20020137127A1
; GENERAL INFORMATION:
; APPLICANT: Moore et al.
; TITLE OF INVENTION: Human FK506 Binding Proteins
; FILE REFERENCE: PF392
; CURRENT APPLICATION NUMBER: US/09/225,502A
; CURRENT FILING DATE: 1999-01-06
; PRIOR APPLICATION NUMBER: 60/070,875
; PRIOR FILING DATE: 1998-01-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 8
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-225-502-8

Query Match 52.6%; Score 1606; DB 10; Length 388;
Best Local Similarity 98.1%; Pred. No. 8.3e-133;
Matches 302; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 195 TVYIGWLIPGMDKGLGKVCGERKIIITIPPLAYGEDGDKDIPQASLVFDVALLDLH 254
Db 1 TYGEIGWLIPGMDKGLGKVCGERKIIITIPPLAYGEDGDKDIPQASLVFDVALLDLH 60
Qy 255 NPKDSISIKNVVPCNCERISQSGDLTYHYNGTLLDGLTLPDSSYSRNRFTFTYIGQYV 314
Db 61 NPKDSISIKNVVPCNCERISQSGDLTYHYNGTLLDGLTLPDSSYSRNRFTFTYIGQYV 120
Qy 315 IPGMDGGLGVCIGKRXIVPPHLYGEGRGNTIPGSAVLVFDIHDVFNPSDSISIT 374
Db 121 IPGMDGGLGVCIGKRXIVPPHLYGEGRGNTIPGSAVLVFDIHDVFNPSDSISIT 180
Qy 375 SHYKPPDCSVLSKGGDKYKHYNASLLDGLTLDSTWNLGKTYNVLGSGQVVLGMDMGLR 434
Db 181 SHYKPPDCSVLSKGGDKYKHYNASLLDGLTLDSTWNLGKTYNVLGSGQVVLGMDMGLR 240
Qy 435 EMCVGEKRTVIIPPHLYGEGAGVDGPGSAVLVFDIEXLELVAGLPEGYMFIMNGEVP 494
Db 241 EMCVGEKRTVIIPPHLYGEGAGVDGPGSAVLVFDIEXLELVAGLPEGYMFIMNGEVP 300
Qy 495 NLFEEDK 502
Db 301 NLFEEDK 308

RESULT 3

US-09-225-502-4
; Sequence 4, Application US/09225502A
; Patent No. US20020137127A1
; GENERAL INFORMATION:
; APPLICANT: Moore et al.
; TITLE OF INVENTION: Human FK506 Binding Proteins
; FILE REFERENCE: PF392
; CURRENT APPLICATION NUMBER: US/09/225,502A
; CURRENT FILING DATE: 1999-01-06
; PRIOR APPLICATION NUMBER: 60/070,875
; PRIOR FILING DATE: 1998-01-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 4
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-225-502-4

Query Match 45.8%; Score 1399; DB 10; Length 441;
Best Local Similarity 58.0%; Pred. No. 1.4e-114;
Matches 255; Conservative 77; Mismatches 102; Indels 6; Gaps 4;

Qy 134 FDLVLDIWNSEDQVQIHTYFKBPSCPTIQVSDFVRHYNGTLLDGLTLPDSSHNRKMTY 193
Db 1 FDLVLDIWNKEDTVQVSTLLRPPHPCPRMVGDFVRHYNGTLLDGLTLPDSSHNRKMTY 60
Qy 194 DTYVIGWLIPGMDKGLGKVCGERKIIITIPPLAYGEDGDKDIPQASLVFDVALLDL 253
Db 61 DTYVIGWLIPGMDKGLGKVCGERKIIITIPPLAYGEDGDKDIPQASLVFDVALLDL 120
Qy 254 HNPKDSISIKNVVPCNCERISQSGDLTYHYNGTLLDGLTLPDSSYSRNRFTFTYIGQY 313
Db 121 HNPKDSISIKNVVPCNCERISQSGDLTYHYNGTLLDGLTLPDSSYSRNRFTFTYIGQY 180
Qy 314 VIPGMDGGLGVCIGKRXIVPPHLYGEGRGNTIPGSAVLVFDIHDVFNPSDSIS 372
Db 181 VIPGMDGGLGVCIGKRXIVPPHLYGEGRGNTIPGSAVLVFDIHDVFNPSDSIS 240
Qy 373 ITSHYKPPDCSVLSKGGDKYKHYNASLLDGLTLDSTWNLGKTYNVLGSGQVVLGMDM 431
Db 241 ITSHYKPPDCSVLSKGGDKYKHYNASLLDGLTLDSTWNLGKTYNVLGSGQVVLGMDM 300
Qy 432 GLREMCVGEKRTVIIPPHLYGEGAGVDGPGSAVLVFDIEXLELVAGLPEGYMFIMNGE 491
Db 301 GLREMCVGEKRTVIIPPHLYGEGAGVDGPGSAVLVFDIEXLELVAGLPEGYMFIMNGE 359
Qy 492 VSPNLFEEIDKNGEVLLEFSEYIHAQVAGSKGLAPGDAELIVKMTNQRNGDG 551
Db 360 VSPNLFEEIDKNGEVLLEFSEYIHAQVAGSKGLAPGDAELIVKMTNQRNGDG 419
Qy 552 KVTAEEFKL---XDOEAH 568
Db 420 KVTAEEFKL---XDOEAH 439

RESULT 4

US-09-225-297-808
; Sequence 808, Application US/09925297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA105
; CURRENT APPLICATION NUMBER: US/09/925,297
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05989
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 808

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; LENGTH: 434
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-297-808

Query Match 44.3%; Score 1354; DB 10; Length 434;
Best Local Similarity 57.5%; Pred. No. 1.3e-110;
Matches 249; Conservative 76; Mismatches 102; Indels 6; Gaps 4;

QY 141 INWSEDOQIHYTFKPPSPRTIQVSDFYRYHYNGTFLDGTFLDSSSHNMKTYDTYVVGIG 200
DB 1 IRHEEDTVQVSTLLRPPHPCPRVQDGFVRYHYNGTLLDGTSDFTSYSGKGTDTYVVGSG 60

QY 201 WLPMDKGLGMCVGEKRIITIPPLAYGEDGDKDIPQASLVFDVALLDHPKDSI 260
DB 61 WLIKMDQGLGMCVGERKRIITIPPLAYGEKGYGTVIPQASLVFHVLLIDVHNPDAV 120

QY 261 SIENKVPENCERISQSGDPLTVHYNGTLLDGTFLDSSYSRNRTPDTYIGQGVIPGMD 320
DB 121 QLETLPPGCVRRAGAGDFMRHYNGSLMDGTLFDSSYSRNMITYIYIGQGVIIQMDQ 180

QY 321 GLLGVCIGEKRIIVPPHLYGEGEGN-IPGSAVLVFDIHDVFNPSDSISITSHYKP 379
DB 181 GLQGCWGERRITIPPLAYGEGTGDKIPGSAVLVFNHVIDFHPADVVEIRLSRP 240

QY 380 PD-CSVLSKGDYKHYNASLLDGTLLDSTWNLGKTYNIVLGSQGVVLGMDGLREMCV 438
DB 241 SETCNETKLGDFVRYHYNGSLDGTQLFTSHDYGAPEATLGANKVIEGLDTGLQMCV 300

QY 439 GEKRTVIPPGLGYGAGVDGVPVGSALVFDIEXLELVAGLPEGYMFIWNGEVSNNLFE 498
DB 301 GERQLIVPPLHAGSGARG-VPGSAVLVFEVELVSREGLTGTGLVFWHKDPPANLFE 359

QY 499 EIDKQNGEVLLEPFSYIHAQVASKGLAPGDAELIVKNMFTNQDRNGDKGVTAEEF 558
DB 360 DMLNDKDGVEPPEFSFTFIKAQVSEKGRMLPGQDPEKTIQDMFQNDQNGDKITVDEL 419

QY 559 KL---XDQEAHID 568
DB 420 KLKSDDEERHVE 432

RESULT 5
US-09-925-300-1692
; Sequence 1692, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Steve Ruben,
; APPLICANT: Craig Rosen,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1692
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1692

Query Match 24.3%; Score 743; DB 10; Length 366;
Best Local Similarity 43.5%; Pred. No. 4e-57;
Matches 165; Conservative 45; Mismatches 91; Indels 78; Gaps 10;

; LENGTH: 434
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-297-808

Query Match 44.3%; Score 1354; DB 10; Length 434;
Best Local Similarity 57.5%; Pred. No. 1.3e-110;
Matches 249; Conservative 76; Mismatches 102; Indels 6; Gaps 4;

QY 141 INWSEDOQIHYTFKPPSPRTIQVSDFYRYHYNGTFLDGTFLDSSSHNMKTYDTYVVGIG 200
DB 1 IRHEEDTVQVSTLLRPPHPCPRVQDGFVRYHYNGTLLDGTSDFTSYSGKGTDTYVVGSG 60

QY 201 WLPMDKGLGMCVGEKRIITIPPLAYGEDGDKDIPQASLVFDVALLDHPKDSI 260
DB 61 WLIKMDQGLGMCVGERKRIITIPPLAYGEKGYGTVIPQASLVFHVLLIDVHNPDAV 120

QY 261 SIENKVPENCERISQSGDPLTVHYNGTLLDGTFLDSSYSRNRTPDTYIGQGVIPGMD 320
DB 121 QLETLPPGCVRRAGAGDFMRHYNGSLMDGTLFDSSYSRNMITYIYIGQGVIIQMDQ 180

QY 321 GLLGVCIGEKRIIVPPHLYGEGEGN-IPGSAVLVFDIHDVFNPSDSISITSHYKP 379
DB 181 GLQGCWGERRITIPPLAYGEGTGDKIPGSAVLVFNHVIDFHPADVVEIRLSRP 240

QY 380 PD-CSVLSKGDYKHYNASLLDGTLLDSTWNLGKTYNIVLGSQGVVLGMDGLREMCV 438
DB 241 SETCNETKLGDFVRYHYNGSLDGTQLFTSHDYGAPEATLGANKVIEGLDTGLQMCV 300

QY 439 GEKRTVIPPGLGYGAGVDGVPVGSALVFDIEXLELVAGLPEGYMFIWNGEVSNNLFE 498
DB 301 GERQLIVPPLHAGSGARG-VPGSAVLVFEVELVSREGLTGTGLVFWHKDPPANLFE 359

QY 499 EIDKQNGEVLLEPFSYIHAQVASKGLAPGDAELIVKNMFTNQDRNGDKGVTAEEF 558
DB 360 DMLNDKDGVEPPEFSFTFIKAQVSEKGRMLPGQDPEKTIQDMFQNDQNGDKITVDEL 419

QY 559 KL---XDQEAHID 568
DB 420 KLKSDDEERHVE 432

RESULT 6
US-09-225-502-2
; Sequence 2, Application US/09225502A
; Patent No. US20020137127A1
; GENERAL INFORMATION:
; APPLICANT: Moore et al.
; TITLE OF INVENTION: Human FK506 Binding Proteins
; FILE REFERENCE: PF392
; CURRENT APPLICATION NUMBER: US/09/225,502A
; CURRENT FILING DATE: 1999-01-06
; PRIOR APPLICATION NUMBER: 60/070,875
; PRIOR FILING DATE: 1998-01-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-225-502-2

Query Match 24.1%; Score 737; DB 10; Length 336;
Best Local Similarity 58.1%; Pred. No. 1.2e-56;
Matches 140; Conservative 35; Mismatches 50; Indels 16; Gaps 3;

QY 10 PP-----PLLLLLWVT-----GQAAPVAGLGSDELQIERRFVDECPRTVRS 55
DB 6 PPSHLLRLPLQLLLVQAVGRGLGRASPAGGPLED--VWIERYHIPRACPREVQWD 63

QY 56 FVRYHYVTGPDGOKFSDSYDRDSTFNVFGKGLITGMDQALVCMCNERRFVKIPKL 115
DB 64 FVRYHYNGTGEDGKFDSSYDRNTLVVAIVGVGLIITGMDRGLMCMCNERRLIIVPHL 123

QY 116 AYGNERSVGVIPNPSVLHFDVLLMDIWNSEDOQIHYTFKPPSPRTIQVSDFYRYHYNG 175
DB 124 GYSGISGLAGLIPPDATLVFDVLLDVNKKEDTVQVSTLLRPPHPCPRVQDGFVRYHYNG 183

QY 176 TFLDGTFLDSSSHNMKTYDTYVVGIGLIPGMDKGLGMCVGEKRIITIPPLAYGEDG 235
DB 184 TLLDGTSDFTSYSGKGTDTYVVGSGWLIKMDQGLGMCVGERKRIITIPPLAYGEKGYG 243

QY 236 K 236
DB 244 E 244
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RESULT 8
US-10-006-818A-180
; Sequence 180, Application US/10006818A
; Publication No. US20030054406A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Hurrey, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.

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Query Match      8.8%; Score 268; DB 9; Length 222;
Best Local Similarity 31.2%; Pred.No. 9.2e-16;
Matches 64; Conservative 44; Mismatches 77; Indels 20; Gaps
Qy 368 SDSISITSHYKPPDCSVLSKKGDYLYKHVNASLL-DGT--LDSTWNLGKTYNVLGSGQ 424
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 32 TEEVKI EVLWRPENCSTKTSKGGDLLNAHYDGYLAKGSGKFYCSRTONEGHPKWFVLGSGQ 91

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QY 425 VVLGMDMLGRLCVMGKERTVIIPPHLGYGEAG-VDEVPVGSVAVLVDIEXLVLVAGLPEG 483
Db 143 VVLGMDMLGRLCVMGKERTVIIPPHLGYGEAG-VDEVPVGSVAVLVDIEXLVLVAGLPEG 483
Db 92 VIKGLDIAMTDCMCPGKVPVPSFAYGKEGAEKIPPDATLIFEI---ELVA----- 143
QY 484 YMFVNGEVSPLFREIDKNGEVLLEBFSEVHIAQVASKGLAPGPDASLIVKNMPT 543
Db 144 ---VTKGPRSIETFKQIDMNDNRQJSKAEINLYLOREFEKDKPRDKSQ-DAVLEDIPK 199
QY 544 NDRNGDGKVTABEFLKXDOEARHD 568
Db 200 KNDHGDGDFISPKYNNV-----QHD 220

RESULT 10
US-09-946-374-180
; Sequence 180, Application US/09946374
; Publication No. US20030073129A1
GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Fertara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
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; PRIOR APPLICATION NUMBER: 60/099536
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;; PRIOR APPLICATION NUMBER: 60/103314
;; PRIOR FILING DATE: 1998-10-07
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;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103328
;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103395
;; PRIOR FILING DATE: 1998-10-07
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;; PRIOR FILING DATE: 1998-10-22
;; PRIOR APPLICATION NUMBER: 60/105693
;; PRIOR FILING DATE: 1998-10-26
;; PRIOR APPLICATION NUMBER: 60/105694
;; PRIOR FILING DATE: 1998-10-26
;; PRIOR APPLICATION NUMBER: 60/105807

Query Match 8.8%; Score 268; DB 9; Length 222;
Best Local Similarity 31.2%; Pred. No. 9.2e-16;

Matches 64; Conservative 44; Mismatches 77; Indels 20; Gaps 7;
QY 368 SDSISITSHYKPPDCSVLSKKGYLKYHYNASLL-DGT--LLDSTWNLGKTYNIVLGSQ 424
DB 32 TEEVKIEVLHREPENCSTSKKGLLNNAHYDGYLAKDGSKFYCSRTQNEGHPKWFVLGVGQ 91
QY 425 VVLGMDMGLREMCVGEKRTVIIPPHLGYGEAG-VDGEVPGSAVLVFDITEXLELVAGLPEG 483
DB 92 VIKGLDIAMTDMCPGKRRKVVIPPSFAYGEGYAEKIPPDATLIFEI---ELYA----- 143
QY 484 YMFVINGEVSPNLFEEIDKNGEVLLEEFSEYTHAQVASKGLAPGFDALIVKNMFT 543
DB 144 ---VTKGRPSITETFKQIDMDNDRLSKABINLYLQREFEKDEKPRDKSYQ-DAVLEDFK 199
QY 544 NQDRNGDGKVTAEERFKLXQEAHD 568
DB 200 KNDHGDGDFISPKYNNY----QHD 220

RESULT 11

US-10-012-121A-180
; Sequence 180, Application US/10012121A
; Publication No. US20030073810A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Denoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC20
; CURRENT APPLICATION NUMBER: US/10/012,121A
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 180
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-121A-180

Query Match 8.8%; Score 268; DB 9; Length 222;

Best Local Similarity 31.2%; Pred. No. 9.2e-16;
Matches 64; Conservative 44; Mismatches 77; Indels 20; Gaps 7;

QY 368 SDSISITSHYKPPDCSVLSKKGYLKYHYNASLL-DGT--LLDSTWNLGKTYNIVLGSQ 424
DB 32 TEEVKIEVLHREPENCSTSKKGLLNNAHYDGYLAKDGSKFYCSRTQNEGHPKWFVLGVGQ 91
QY 425 VVLGMDMGLREMCVGEKRTVIIPPHLGYGEAG-VDGEVPGSAVLVFDITEXLELVAGLPEG 483
DB 92 VIKGLDIAMTDMCPGKRRKVVIPPSFAYGEGYAEKIPPDATLIFEI---ELYA----- 143
QY 484 YMFVINGEVSPNLFEEIDKNGEVLLEEFSEYTHAQVASKGLAPGFDALIVKNMFT 543
DB 144 ---VTKGRPSITETFKQIDMDNDRLSKABINLYLQREFEKDEKPRDKSYQ-DAVLEDFK 199
QY 544 NQDRNGDGKVTAEERFKLXQEAHD 568
DB 200 KNDHGDGDFISPKYNNY----QHD 220

RESULT 12


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US-10-015-869A-180
; Sequence 180, Application US/10015869A
; Publication No. US20030073130A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PIC45
; CURRENT APPLICATION NUMBER: US/10/015,869A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 180
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-869A-180

Query Match      8.8%; Score 268; DB 9; Length 222;
Best Local Similarity 31.2%; Pred. No. 9.2e-16;
Matches 64; Conservative 44; Mismatches 77; Indels 20; Gaps 7;

QY 368 SDSISITSHYKPPDCVLSKKGDLKHYNNASLL-DGT--LLDSYTNLGTNYNVLGSGQ 424
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
32  TEVKLEVLHRPNCSTSKGDLNNAHYDGLAKDGSKFYCSRTQNEGHPKFWVLGVGQ 91
QY 425 VVLGMDMGLREMCVGKRTVIIPHLGYBAG-VDGVPVGSVAVLFDIEKLEVLAVGLPEG 483
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
92  VIKGLDIAMTDCGPKRKKVIPPSPAYKGEQVAGKIPDPATLIFEI---ELVA----- 143
QY 484 YMIWNGEVSFNLFEETDKDNGEVLLEESFYIHAQVASKGKLAPGDAELIVKNMET 543
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
144 ---VTGPRSIETFKQIDMDNDQLSKAEINLYLQREFEKDEKPRDKSYQ-DAVLIEDIFK 199
QY 544 NQDRNGDGKVTABEFKLKQDAKH 568
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
200 KNDHGDGDFISPKYNYV---QHD 220

RESULT 13
US-09-978-295A-145
; Sequence 145, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
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;; PRIOR FILING DATE: 1998-04-01
;; PRIOR APPLICATION NUMBER: 60/080328
;; PRIOR FILING DATE: 1998-04-01
;; PRIOR APPLICATION NUMBER: 60/080333
;; PRIOR FILING DATE: 1998-04-01
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;; PRIOR FILING DATE: 1998-05-15
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Query Match 8.4%; Score 256; DB 9; Length 211;

Best Local Similarity 33.0%; Pred. No. 9.7e-15;

Matches 73; Conservative 38; Mismatches 88; Indels 22; Gaps 7;

Qy 352 SAVL-VFDIHVIDFHPNPSDSISITSHYKPPDCSVLSKGDYLVKHYNASL-LDGTLLDST 409

Db 7 NAVLTFTVSLIGALIPPEPEVKIEVLQPFICHRKTKGDLMLVHYEGYLENDGSLFHS 66

Qy 410 --WNLGKTYNIVLGSQVVLGMDMLGMLREMCVGEKRTVII PHLGVYGEAGVDGVEPGSAVL 467

Db 67 HKHNGQPIWFTLGLILEALKWDQGLKGMVCGERKLLIIPALGYKKG-KGKIPPESTL 125

Qy 468 VFDIEXLELVAGLPEGYMFVWNGEVSPLFEIDKDGNGEVLLFEFSYTHAQVASGK 527

Db 126 IFNIDLLLE-----IRNGPRSHESFQEMDLNDMDKLSKDEVKAYLKKEPEK-HGA 173

Qy 528 LAPGFDALIVKNMFTNODRNGDKVTAEEFKLXDOEAKHD 568

Db 174 VNESHHDALVEDIFDKEDDKDGFISAREFTY-----KHD 209

RESULT 14

US-09-978-697-145

Sequence 145; Application US/09978697

Patent No. US20020169284A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
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PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366

APPLICANT: Filvaroff, Ellen	APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang	APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.	APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.	APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.	APPLICANT: Hillan, Kenneth J.
APPLICANT: Klijavin, Ivar J.	APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.	APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.	APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.	APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel	APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.	
TITLE OF INVENTION: Acids Encoding and Translating	
FILE REFERENCE: P2630PlC9	
CURRENT APPLICATION NUMBER: US/09/97	
PRIOR APPLICATION NUMBER: 2001-10-15	PRIOR APPLICATION NUMBER: 09/9148585
PRIOR FILING DATE: 2001-07-30	PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17	PRIOR APPLICATION NUMBER: 60/064249
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PRIOR FILING DATE: 1998-03-30	PRIOR APPLICATION NUMBER: 60/079923

Matches 73; Conservative 38; Mismatches 88; Indels 22; Gaps 7;

7 NAYI TEI EUEEOT TCAI T DECEBET EIB OYDET CUBVYVZCOOI MT ITNTECVY EYBDOOY EYBDOOY

QY 410 --WNLGKTYNIVLGSGQVVLGMDMGLREMCVGEKRTVII PPHLGYGEAGVDGEVPGSAVL 467

100

db 126 IFNIDLE-----IRNGPRSHESFQEMDLNDDWKLKSKDEVKAYLKKEFEK-HGA 173

323 3A4F0F0A8E11V4NMJF1N0Q4NGDGRV1AE0F1N4DQEAAND 368

US-09-978-192A-145

Patent No. US20020177553A1
GENERAL INFORMATION:

APPLICANT: Baker Kevin p

APPLICANT: Eaton, Dan

; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/080105
; PRIOR FILING DATE: 1998-03-31
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; PRIOR APPLICATION NUMBER: 60/083500
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; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 8.4%; Score 256; DB 9; Length 211;

Best Local Similarity 33.0%; Pred. No. 9.7e-15;

Matches 73; Conservative 38; Mismatches 88; Indels 22; Gaps 7;

QY 352 SAVL-VFDIHVIDFHNPSDSISITSHYKPPDCSVLSKGDYLYKHYNASL-LDGTLLDST 409
Db 7 NAVTLFVTSLIGALPEPEVKIEVLQKPFICHRKTKGGDLMLVHYEGYLEKDGSLFHST 66
QY 410 --WNLGKTYNIVLGGQGVILGMDGLREMCVGERKTVIIPPHLGYGAGVDGVPGSAVL 467
Db 67 HKHNNQPIWFTLIGLEALKGWDQGLKGMVCVGERKLIIPALGYGKEG-KGKIPPESTL 125
QY 468 VFDIEXLELVAGLPEGYMFTWNGEVSFNLFEEDKDGNGEVILLEEFSEYIHAQVASCKGK 527
Db 126 IFNIDLE-----IRNGPRSHESFOEMDLNDWKLSDKDEVKAYLKKEFEK-HGA 173
QY 528 LAPGFDAELIVKNMFTNQDRNGDGKVTAEFFKLXDQBAKHD 568
Db 174 VNESHHDALVEDIFDKEDKDGFIARBEFTY-----KHD 209

Search completed: April 26, 2003, 07:06:37

Job time : 20.1541 secs

GenCore version 5.1.4 p5.4578
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OM protein - protein search, using sw model

Run on: April 26, 2003, 06:48:54 ; Search time 18.1541 Seconds
(without alignments)
3039.596 Million cell updates/sec

Title: US-09-225-502-6

Perfect score: 3054

Sequence: 1 MAFGRWRPPPPPLLLLLLMV.....ABEFKLXQKAKHDVTNLNA 574

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 73.*

1: Pirl.*

2: Pirl.*

3: Pirl.*

4: Pirl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1750.5	57.3	581	2 149669	FKBP65 binding prote
2	736	24.1	262	2 T42709	hypothetical prote
3	382	12.5	559	1 S55383	peptidylprolyl iso
4	344.5	11.3	261	2 T31741	hypothetical prote
5	343	11.2	264	2 T29780	hypothetical prote
6	311	10.2	551	1 S72485	peptidylprolyl iso
7	307	10.1	568	2 T06489	probable peptidylp
8	294.5	9.6	259	2 T27586	hypothetical prote
9	286.5	9.4	139	2 T21882	hypothetical prote
10	266.5	8.7	241	2 E89251	protein 2C455.10 (
11	263.5	8.6	311	1 A46228	peptidylprolyl iso
12	263	8.6	151	2 T12090	probable peptidylp
13	262.5	8.6	304	2 T26538	hypothetical prote
14	259.5	8.5	163	2 S71238	probable peptidylp
15	254.5	8.3	134	1 J70748	FK506-binding prot
16	253	8.3	146	1 S71237	probable peptidylp
17	246	8.1	140	2 I49668	binding protein -
18	244.5	8.0	135	2 S25337	peptidylprolyl iso
19	242.5	7.9	142	2 J1365	FK506/rapamycin-bi
20	230.5	7.5	120	2 S11090	FK506-binding prot
21	228	7.5	458	1 A42386	hsp 90-binding prot
22	228	7.5	459	2 A46372	immunophilin FKBP5
23	223	7.3	458	2 JN0873	immunophilin p59 -
24	217	7.1	457	2 J05422	FK506-binding prote
25	214.5	7.0	113	2 A83180	probable peptidylp
26	212.5	7.0	165	2 A81878	FKBP-type peptidyl
27	211.5	6.9	201	1 S75144	FKBP-type peptidyl
28	208	6.8	152	2 B75347	peptidyl-prolyl ci
29	207	6.8	114	2 A33146	peptidylprolyl iso

ALIGNMENTS

RESULT 1

I49669

FKBP65 binding protein - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999

C:Accession: I49669

R:Simsek, S.L.; Kozak, C.A.; Winterstein, D.; Hegamyer, G.; Colburn, N.H.

Genomics 18, 407-409, 1993

A>Title: Sequence and localization of a novel FK506-binding protein to mouse chromosomes

A:Reference number: A48920; MUID:94117013; PMID:7507077

A:Accession: I49669

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-581 <RES>

A:Cross-references: GB:L07063; NID:g894161; PIDN:AAC37678.1; PID:g894162

C:Superfamily: BKBP-type peptidylprolyl isomerase homology

F:61-108/Domain: BKBP-type peptidylprolyl isomerase homology <PPI1>

F:173-220/Domain: BKBP-type peptidylprolyl isomerase homology <PPI2>

F:285-332/Domain: BKBP-type peptidylprolyl isomerase homology <PPI3>

F:398-445/Domain: BKBP-type peptidylprolyl isomerase homology <PPI4>

Query Match 57.3%; Score 1750.5; DB 2; Length 581;
Best Local Similarity 58.9%; Pred. No. 3.8e-118;
Matches 333; Conservative 90; Mismatches 131; Indels 11; Gaps 7;

QY	12	PLLLLLLMV---TGQAAPVAGLSDAELQIERFVDECPRTVRSQDFVRYHYVGTTPDG	68
DB	18	PLLLLLQTLERGLGRASP-AGAPLE-DWIERVHI PRACPVEQMGDFVRYHYNGTPEDG	75
QY	69	QKFDSSYDRDSTFNVFVGKGLITGMDQALVGCNERRFVKIPPKLAYGNERSGVITPP	128
DB	76	KKFDSSYDRSTLVAIVVGVGRLLITGMDRLGMLGCNERRRLIVPPLHLYGSGVAGLIPP	135
QY	129	NSVLHPDVLMDIWNSEDQVQIHTYFKPPSCPTIQVDFRVHYNGTFLDGLTDFDSSH	188
DB	136	DATLYFDVLLDWNKADTVQSTILLRPPYCPRMVQNSDFRVHYNGTLLDGTGFDNSYS	195
QY	189	RMKTYTYVIGIWLIPGMDKGLGMCVGEKRIITIPPLAYGEDGDGKDIPQASLVFDV	248
DB	196	RGTTYDTYIGSGWLIKGMDQGLLGMCPGEKRIIPPLAYGEGYGTVIPQASLVFV	255
QY	249	ALLDLNPKDSISIEKNKVPENCERISQSGDLTYHYNGTLLDGLTDFDSSYSRRTPTD	308
DB	256	LLLDVHNPKDTVQLETLELPQGCVRRAVAGDFMRHYNGSLMDGTDFDSSYSRHNNTY	315
QY	309	IGQGYVYIPGMDGLLVCIGEKXIVVPPHLGVEEGRGN-IPGSALVLFDFHIDFNP	367
DB	316	VGQGYIIPGMDQGLQACIGERRITVPPHLYGENTGDKIPGSALVLFDFHIDFNP	375
QY	368	SDSISITSHYKPPD-CSVLSSKGDYLYKHYNASLLDGLTLLDSTWNLGKTYNVLGSGQV	426
DB	376	SDPVEIKTLSPENCNCTSKIGDFIRHYNCSLLDGLTRLPFSSHDEAPQBITLCAKVI	435

QY 427 LGMGLREMVCGERKTVIIPPHLYGAGVDGVPVGSVAVLFDIEXLELVAGLPEGYMF 486
 Db 436 EGLDGLGCMVGERRQLIIPPHLAHSGARG-VPGSAVLLEFVELSRDEGLPTGYLF 494
 QY 487 IWNGEVSNNLFEIDKNGEVLLEEFSEYTHAQVASKGKLAGPDAELIVKNNFTNQD 546
 Db 495 VVYQDPSTLFDMDLNKGDEVPPEEFSSFIKAQVNEKGRLMPQDPDKTISDMFQND 554
 QY 547 RNDGKVTAEFKL---XDQEAHND 568
 Db 555 RNQDKITAEELKLKSDDEQVRVHE 579

RESULT 2

T42709

Hypothetical protein DKFZp586I0821.1 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 02-Sep-2000

C;Accession: T42709

R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, November 1999

A;Reference number: Z22231

A;Accession: T42709

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-262 <AAA>

A;Cross-references: EMBL:AL131116

A;Experimental source: adult uterus; clone DKFZp586I0821

C;Genetics:

A;Note: DKFZp586I0821.1

C;Superfamily: BKBP-type peptidylprolyl isomerase homology

F;79-126/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>

Query Match 24.1%; Score 736; DB 2; Length 262;

Best Local Similarity 52.5%; Pred. No. 1.3e-45;

Matches 137; Conservative 53; Mismatches 65; Indels 6; Gaps 4;

QY 313 YVTPGMDGLGVCIGEKRIIVPPHLYGEGRGN-IPGSAVLVFDIHDHNPDSI 371
 Db 1 YIIPGMDQGLGACMGERRITIPPHLYGENGTGDKIPGSAVLIFNVHVIDFNPADV 60
 QY 372 SITSHYKPPD-CSVLKGGDYLYKHYNASLLDGTLLSTWNGLKTYNIVLGGQVILGMD 430
 Db 61 EIKTLRSPSETCNETTKLGDVRYHYNCSLDGTQLFTSHDYGAPQBATLCAKAVIEGLD 120
 QY 431 MGLREMCVGEKRTVIIPPHLYGAGVDGVPVGSVAVLFDIEXLELVAGLPEGYMFVWG 490
 Db 121 TGLQCMVGERRQLIIPPHLAHSGARG-VPGSAVLLEFVELSRDEGLPTGYLFVWHK 179
 QY 491 EVSPNLFEEIDKNGEVLLEEFSEYTHAQVASKGKLAGPDAELIVKNNFTNQDRNGD 550
 Db 180 DPNANLFEDMDLNKGDEVPPEEFSTFIKAQVSEKGRMLMPQDPEKTIGDMFQNDNRQD 239
 QY 551 GKVTAEFKL---XDQEAHND 568
 Db 240 GKITVDELKLKSDDEQVRVHE 260

RESULT 3

S55383

peptidylprolyl isomerase (EC 5.2.1.8) - wheat

N;Alternate names: FK506-binding protein; peptidylprolyl cis-trans isomerase; PPIase

C;Species: Triticum aestivum (common wheat)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000

C;Accession: S55383

R;Oshra, B.; Breiman, A.

submitted to the EMBL Data Library, May 1995

A;Description: Wheat FKBP70 - A novel heat shock and calmodulin binding PPIase.

A;Reference number: S55383

A;Accession: S55383

A;Molecule type: mRNA

A;Residues: 1-559 <OSH>

A;Cross-references: EMBL:X86903; NID:g854625; PIDN:CAA60505.1; PID:g854626
 C;Genetics:

A;Gene: FKBP70

C;Superfamily: peptidylprolyl isomerase ROP1; BKBP-type peptidylprolyl isomerase hom
 C;Keywords: calmodulin binding; cis-trans isomerase; cyclosporin A binding
 F;60-107/Domain: BKBP-type peptidylprolyl isomerase homology <PPI1>
 F;176-219/Domain: BKBP-type peptidylprolyl isomerase homology <PPI2>
 F;1293-341/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>
 F;415-448/Domain: tetratricopeptide repeat homology <TT1>
 F;450-483/Domain: tetratricopeptide repeat homology <TT2>
 F;484-517/Domain: tetratricopeptide repeat homology <TT3>

Query Match 12.5%; Score 382; DB 1; Length 559;

Best Local Similarity 30.1%; Pred. No. 1e-19;

Matches 113; Conservative 54; Mismatches 166; Indels 42; Gaps 11;

QY 50 TVRSGDFVRYHYVGFPGQKFDSSVDRDSTFNVFVGKQLITGMDOALVGMCVNERFV 109
 Db 56 TPEVGEVEVHTGTLLDGKFDSSRDRTDFKFLGQGVKGVGOGIKTMKKGENALF 115
 QY 110 KIPPKLAYGNERSGVIPPNLSVLFHFDVLLMDIWNSEDQVQIHTYFKP-----PSC 159
 Db 116 TIPPELAYGESGSPPTIPANATLQFDVELLSWTSVRDIAKGGGIFKKILKEGDKWENPKD 175
 QY 160 PRTIQVSDFVRYHYNGTFLDGTLPDSSHNRMKTYTYVIGWLIIPGMDKGLLGMVCVEKR 219
 Db 176 P-----DEVFVKYEARLEDGTWVSKSEG----VEFTVKDGHLCALAKAVTKMKGEKV 225
 QY 220 IITIPPFLAYGE-----DQDGDKDIQQAASLVDFDVALLD---LHNPKDSISIEKVVPP--E 269
 Db 226 LLAVKPOYGFGEGRPAAGEGAVPNASLVLDLSELVSWKTVTTEIGDDKKILKKVLKEXE 285
 QY 270 NCRISQSGDFLTTHYNGTLLDGTLP-DSSVSRNRTFTYIQGVYIPGMDEGLLGVCI 328
 Db 286 GYERFNE-GAVTVTKITGLQDGTFLKKGHDQEPFPEKTDDEAVIEGLDRAVLNKKG 344
 QY 329 EKRXIVPEPHLYGGE-EGRGN--IPGSAVLVFDIHDHNPDSISITSH-----YK 378
 Db 345 EVALVTIPPEYAYGSTESKQDAIVPNSTVIYVELSVFVKDESWDLNNSKEIAAGTK 404
 QY 379 PPDCSVLSKKGDIYK 393
 Db 405 KEEGNALFKSGKYAR 419

RESULT 4

T31741

hypothetical protein C05C8.3 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 02-Sep-2000

C;Accession: T31741

R;Sammons, L.; Wohldmann, P.

submitted to the EMBL Data Library, July 1997

A;Description: The sequence of C. elegans cosmid C05C8.

A;Reference number: Z21078

A;Accession: T31741

A;Status: preliminary; translated from GE/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-261 <SAM>

A;Cross-references: EMBL:AF016430; PIDN:AAB65370.1; GSPDB:GN00023; CBSP:C05C8.3

A;Experimental source: strain Bristol N2; clone C05C8

C;Genetics:

A;Gene: CBSP:C05C8.3

A;Map position: 5

A;Introns: 119/3

C;Superfamily: BKBP-type peptidylprolyl isomerase homology

F;48-94/Domain: BKBP-type peptidylprolyl isomerase homology <PPI1>

F;166-213/Domain: BKBP-type peptidylprolyl isomerase homology <PPI2>

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

Length

Pred. No.

<OSH>

Db 34 ITTSSIDESCEIKSAGDVVDQYKLTDEKGVIGSNFGK-KPYTFTLGRNQVIPGMD 92
QY 320 EGLLGVICIGKRXIVPPHLCYGEGRNIPGSAVLVDIHDVDFH--NP-----SDSI 371
Db 93 RAMGMCIGERIKRVIPPKVGFADKSTCQ-----PLYTVQLVNLFRANPGRWTEBGI 147
QY 372 SITSHYK-PPDCSVLSKGDYKHYNASLLDGTLLDSTWNLGKTYNIVLGSQVVLGMD 430
Db 148 QIDQIHKEADCKKAEAGDKIYQOYVLRLEDNTL-----EVIDGMD 189
QY 431 MGLREMCGEKRTVILPHLGYGAGVDGEPGSAVLVDFDIEXLELV 477
Db 190 IAMDGMCEGERRRVIPSEYGYGSGSPPEIPGGARLFEIVLEKLV 236

RESULT 11

S46228

peptidylprolyl isomerase (EC 5.2.1.8) FKBP-33 precursor - Streptomyces chrysomallus

N;Alternate names: fkbB protein

C;Species: Streptomyces chrysomallus

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C;Accession: S46228

R;Fahl, A.; Keller, U.

EMBO J. 13, 3472-3480, 1994

A;Title: Streptomyces chrysomallus FKBP-33 is a novel immunophilin consisting of two FKs

A;Reference number: S46227; MUID:94341259; PMID:8062824

A;Accession: S46228

A;Molecule type: DNA

A;Residues: 1-311 <PAH>

A;Cross-references: GB:234523; NID:G535270; PIDN:CAA84280.1; PID:G633644

A;Experimental source: ATCC 11523

C;Genetics:

A;Gene: fkbB

C;Superfamily: peptidylprolyl isomerase FKBP33; BKBP-type peptidylprolyl isomerase homol

F;1-18/Domain: blocked amino end; cis-trans-isomerase; lipoprotein

F;19-311/Product: signal sequence #status predicted <SIG>

F;77-125/Domain: BKBP-type peptidylprolyl isomerase FKBP-33 #status predicted <MAT>

F;224-271/Domain: BKBP-type peptidylprolyl isomerase homology <PPI1>

F;19/Modified site: fatty acylated amino end (Cys) (in mature form) #status predicted

F;19/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status predicted

Query Match 8.6%; Score 263.5; DB 1; Length 311;
Best Local Similarity 27.6%; Pred. No. 1.6e-11;
Matches 84; Conservative 49; Mismatches 100; Indels 71; Gaps 11;

QY 212 GMCVGEKRIITIPPLAYGEGDGKDIPGQASLVDFVALLDLHNPKDSISIKVVPENC 271

Db 41 GAKFGEK-----PTLSKGE-GD-----PPKE---LKTDTVISEGD 70

QY 272 ERISQSGDLTYHYNGTLLDGTLL-PDSSYSRNRTPTDTYIGQYVIPGMDGGLGVCIGBK 330

Db 71 GAKLNGDAIQVYLGQAWDSTKPFNSFDRKQPPDLTLAGMVIQGWDKGLVGQKVSGR 130

QY 331 RXIVVPPHLYGEGGRNIPGSAVLVDFIHI-----PPKE---LKTDTVISEGD 362

Db 131 VELVIPPGLGEGGQGDIKENATLVFVVDILKATQIPASAKGTEVAQNDVLPKVGVT 190

QY 363 DFHNPSDSI-----SITSHYKPPDCSVLSKGDYKHYNASLLDGTLLDSTWNLGK 414

Db 191 DGKAPTVPKSDPPKLVNSVLESDEGVVKSDESVVVVYVGMVWKAKBFDNTYITGK 250

QY 415 TYNIVLGSQVVL-GMDNGLREMCGEKRTVILPHLGYGAGVDGEPGSAVLVDFDIEX 473

Db 251 TQTPLP--SQVTLKGLKNGLIDKKVGSRLVILVPPDQAFGQQQQA-IPKNSLTVLFAVDI 307

QY 474 LELV 477

Db 308 LAKV 311

RESULT 12

T12090
probable peptidylprolyl isomerase (EC 5.2.1.8) FKBP15 precursor - fava bean
N;Alternate names: FK506-binding protein; immunophilin; rapamycin-binding protein
C;Species: Vicia faba (fava bean)
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000
C;Accession: T12090
R;Luan, S.; Kudla, J.; Gruissem, W.; Schreiber, S.L.
Proc. Natl. Acad. Sci. U.S.A. 93, 6964-6969, 1996
A;Title: Molecular characterization of a FKBP-type immunophilin from higher plants.
A;Reference number: Z17411; MUID:96293457; PMID:8692927
A;Accession: T12090
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-151 <LUA>
A;Cross-references: EMBL:U52045; NID:G1272409; PIDN:AAC49392.1; PID:G1272410
C;Genetics:

A;Gene: FKBP15

A;Note: Inhibited by immunosuppressant drugs FK506 and rapamycin

C;Superfamily: BKBP-type peptidylprolyl isomerase; BKBP-type peptidylprolyl isomerase

C;Keywords: cis-trans-isomerase; cyclosporin A binding; immunoregulation

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-151/Product: peptidylprolyl isomerase FKBP15 #status predicted <MAT>

F;49-96/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>

Query Match 8.6%; Score 263; DB 2; Length 151;
Best Local Similarity 42.1%; Pred. No. 6.4e-12;
Matches 56; Conservative 22; Mismatches 47; Indels 8; Gaps 3;

QY 244 LVFDV-----ALLDLHNPXD--SISIENKVVPENCERISQSGDLTYHYNGTLLDGTLLFD 296

Db 8 LIPTFIASALVAAKSAADVTELQIGVKYKPASCEVQAHKGDVKVHYRGKLTDTGTVFD 67

QY 297 SSSYSNRRTPTDTYIGQYVIPGMDGGLGVCIGKRXIVVPPHLYGEGGR-GNIPGSAVL 355

Db 68 SSFERNSPDIFELGGQVVKGMWDQGLLMCLGCKRKLKIPAKLGYGSGSPPTIPGGATL 127

QY 356 VFDDHVIDFHNPS 368

Db 128 IFDTELGVNDKS 140

RESULT 13

T26538

hypothetical protein Y18D10A.19b - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 28-Jul-2000

C;Accession: T26538

R;Harris, B.

submitted to the EMBL Data Library, December 1998

A;Reference number: Z20226

A;Accession: T26538

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-304 <WIL>

A;Cross-references: EMBL:AL034393; PIDN:CAA22329.1; CESP:Y18D10A.19b

A;Experimental source: clone Y18D10A

C;Genetics:

A;Gene: CESP:Y18D10A.19b

A;Introns: 82/1; 148/3; 195/1; 262/3

C;Superfamily: BKBP-type peptidylprolyl isomerase homology

F;102-149/Domain: BKBP-type peptidylprolyl isomerase homology <PPI1>

F;216-263/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>

Query Match 8.6%; Score 262.5; DB 2; Length 304;
Best Local Similarity 27.0%; Pred. No. 1.8e-11;
Matches 96; Conservative 43; Mismatches 148; Indels 69; Gaps 9;

QY 129 NSVLHEDVLLMDIWNSEDQVQIHTYFKPSCPRTIQVSDVFRHYNGTFLDGTLLFDSSH 188

Db 5 NGVASTDDSVLPFSWNPVGGQ-----FIVSTYNEYEYKRIFFRELEFGCLLC 51

QY 189 RMKTYDTYVIGWLIPGMDKGLLGMCMVGKRIITIPPLAYGEDGDKDIPGQASLVFDV 248

Db 52 RMRFTNH-----EGMKHLRDHVHVK-----SSCEHEKPKTG----- 85
QY 249 ALLDLHNPXDSISIEKNKVPENCERISQSGDPLTHYNGTLLDGTLPDSSYSRNRFTPTY 308
Db 86 ----IHHQVDKAG--NGVMPEN-----GOLVQCYIEIKLADCYTSWSNYESQNPIIPK 132
QY 309 IGGYVPIPMDEGLLGVICIGEKRXIVPPHGLGYGEEG--RGNIPGSAVLVFDIHFNP 367
Db 133 IGFGEVIPGLDIGIPKMKVGEIATFVSGKYGYGAGFGLIPRNASLTCKVLF----- 187
QY 368 SDSISITSHVK-----PPDCSVLSKKGDYILKYHNASLDGTLDDSTWNLGKTYNI 418
Db 188 --NCSWDSYAKIGVDRQILVQGDNVTKXKQGFTCHYVLVLVDGTAKIDSSRDRETPKF 245
QY 419 VLGSGOVVLGMDGLREMCVGEKRTVLIIPHLGYGEAGVGEVPGSAVLVFDIEXL 474
Db 246 KTGKGEVIGWDQGVQMSVGEKSKLTISADLGYGPRGVPQIPANATLVEVELL 301

RESULT 14

S71238

Probable peptidylprolyl isomerase (EC 5.2.1.8) FKBP15-2 - Arabidopsis thaliana

N;Alternate names: FK-binding protein 15-2; immunophilin

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 16-Jul-1999

C;Accession: S71238

R;Luan, S.; Kudla, J.; Gruissem, W.; Schreiber, S.L.

submitted to the EMBL Data Library, March 1996

A;Description: Molecular characterization of a FKBP-type immunophilin from higher plants

A;Reference number: S71238

A;Accession: S71238

A;Molecule type: mRNA

A;Residues: 1-163 <LUA>

A;Cross-references: EMBL:U52047; NID:g1272407; PIDN:AAC49391.1; PID:g1272408

C;Genetics:

A;Gene: FKBP15-2

C;Superfamily: BKBP-type peptidylprolyl isomerase; BKBP-type peptidylprolyl isomerase ho

C;Keywords: cis-trans-isomerase

F;52-99/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>

Query Match

Best Local Similarity 8.5%; Score 259.5; DB 2; Length 163;

Matches 50; Conservative 15; Mismatches 38; Indels 1; Gaps 1;

QY 260 ISIEKNKVPENCERISQSGDPLTHYNGTLLDGTLPDSSYSRNRFTPTYIGQGYVPGMD 319

Db 34 LQIGVKFKPTCEVQAHKGDTIKVHVGKLTGDFVDSFERGDPFFPKLGGSGQVIKGM 93

QY 320 EGLLGVICIGEKRXIVPPHGLGYGEEGR-GNIPGSAVLVFDIHI 362

Db 94 QGLGACVGEKRLKIPAKLGYEGSGSPPTIPGATLIFDELI 137

RESULT 15

JT0748

FK506-binding protein - Botryllus schlosseri

C;Species: Botryllus schlosseri

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C;Accession: JT0748; S40074

R;Pancer, Z.; Gershon, H.; Rinkevich, B.

Biochem. Biophys. Res. Commun. 197, 973-977, 1993

A;Title: cDNA cloning of a putative protochordate FK506-binding protein.

A;Reference number: JT0748; MUID:94092189; PMID:7505578

A;Accession: JT0748

A;Molecule type: mRNA

A;Residues: 1-134 <PAN>

A;Cross-references: EMBL:X76006; NID:g435470; PIDN:CAA53594.1; PID:g435471

C;Superfamily: BKBP-type peptidylprolyl isomerase; BKBP-type peptidylprolyl isomerase ho

F;41-88/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>

Query*Match

Best Local Similarity 8.3%; Score 254.5; DB 1; Length 134;

Matches 49; Conservative 14; Mismatches 29; Indels 1; Gaps 1;

QY 271 CERISQSGDPLTHYNGTLLDGTLPDSSYSRNRFTPTYIGQGYVPGMDLGLGYCIGBK 330
Db 34 CERKSGGVDLDMHYTGTLEDSKFDSSRRDFTFTTLGGQYVIKGMWDKLLGMCEGER 93
QY 331 RXIVVPPHGLGYGEEGR-GNIPGSAVLVFDIHI 362
Db 94 RKLKIPSDMGYGDGRGSPFPKIPGGATLIFDEVELL 126

Search completed: April 26, 2003, 06:50:55

Job time : 20.1541 secs

GenCore version 5.1.4 p5_4578
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OM protein - protein search, using sw model

Run on: April 26, 2003, 06:48:55 ; Search time 10.2323 Seconds
(without alignments)
2326.688 Million cell updates/sec

Title: US-09-225-502-6

Perfect score: 3054
Sequence: 1 MAFRGWRPPPPPLLLLLLV.....ASEFKLXQBAKHVDVTLNLA 574

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1750.5	57.3	581	1	FKB3_MOUSE Q61576 mus musculus
2	382	12.5	559	1	FKB7_WHEAT Q43207 triticum ae
3	246	8.1	140	1	FKB2_MOUSE P45878 mus musculus
4	244.5	8.0	135	1	FKB2_YEAST P32472 saccharomyc
5	234.5	7.7	217	1	FK21_NEUCR O60046 neurospora
6	231.5	7.6	141	1	FKB2_HUMAN P26885 homo sapien
7	230.5	7.5	120	1	FKB2_NEUCR P20080 neurospora
8	228	7.5	457	1	FKB4_RABIT Q27124 oryctolagus
9	228	7.5	458	1	FKB4_HUMAN Q02790 homo sapien
10	223	7.3	457	1	FKB4_MOUSE P30416 mus musculus
11	217	7.1	457	1	FKB5_HUMAN Q13451 h 51 kda fk
12	210.5	6.9	456	1	FKB5_MOUSE Q64378 mus musculus
13	207	6.8	114	1	FKBP_YEAST P20081 saccharomyc
14	196	6.4	112	1	FKBP_SCHPO O42993 schizosacch
15	195.5	6.4	108	1	FKB1_DROME P48375 drosophila
16	191	6.3	208	1	FKB3_ARATH Q9acy2 arabidopsis
17	184	6.0	268	1	FKBA_AERYH O08437 aeromonas h
18	178	5.8	107	1	FKB1_XENLA O42123 xenopus lae
19	176	5.8	107	1	FKB1_BOVIN P18203 bos taurus
20	174.5	5.7	109	1	FKBP_NEIMA P56989 neisseria m
21	172.5	5.6	107	1	FKB1_RAT Q62658 rattus norv
22	172.5	5.6	109	1	FKBP_NEIMB P25138 neisseria m
23	171.5	5.6	107	1	FKB1_HUMAN P20071 homo sapien
24	171.5	5.6	270	1	FKBA_ECOLI P45523 escherichia
25	171	5.6	205	1	FKBB_ECOLI P39311 escherichia
26	171	5.6	241	1	FKBY_HAETN P44760 haemophilus
27	170	5.6	107	1	FKBB_RAT P97534 rattus norv
28	168	5.5	107	1	FKBB_HUMAN Q16645 homo sapien
29	167	5.5	241	1	FKBA_BUCAL P57599 buchnera ap
30	164	5.4	107	1	FKB1_MOUSE P26883 mus musculus
31	155	5.1	411	1	FKB3_YEAST P38911 saccharomyc
32	154.5	5.1	224	1	FKB3_MOUSE Q62446 mus musculus
33	153	5.0	124	1	FKBP_STRCH P28725 streptomyce

ALIGNMENTS

RESULT 1	FKBX_MOUSE	5.0	224	1	FKB3_BOVIN	P26884 bos taurus
FKBX_MOUSE	153	5.0	243	1	MIP_CHLTR	P26223 chlamydia t
AC	Q61576;	5.0	223	1	FKB3_RABIT	Q06638 oryctolagus
DT	30-MAY-2000 (Rel. 39, Last sequence update)	4.9	224	1	FKB3_HUMAN	Q06688 homo sapien
DT	16-OCT-2001 (Rel. 40, Last annotation update)	4.9	224	1	FKB4_YEAST	Q06205 saccharomyc
DE	65 kDa FK506-binding protein precursor (EC 5.2.1.8) (FKBP65) (FKBPRP)	4.7	392	1	FKB4_CANAL	P28870 candida alb
DE	(Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase)	4.7	124	1	FKB4_DROME	P54397 drosophila
DE	(Immunophilin FKBP65)	4.6	357	1	FKB4_SCHPO	Q74191 schizosacch
GN	FKBP6 OR FKBP1-RS OR FKBP-RS OR FKBP-RP	4.6	361	1	FKB4_SCHPO	Q9PJK1 chlamydia m
OS	Mus musculus (Mouse)	4.5	243	1	MIP_CHLMU	Q10175 schizosacch
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	4.5	362	1	YAV6_SCHPO	O28870 arabidopsis
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	4.4	223	1	FKB3_ARATH	Q927p3 chlamydia p
OX	NCBI_TaxID=10090;	4.4	258	1	MIP_CHLPN	
RN	[1]					
RC	SEQUENCE FROM N.A.					
RP	STRAIN=JBG; TISSUE=Epidermis;					
RX	MEDLINE=94117013; PubMed=7507077;					
RA	Simek S.L., Kozak C.A., Winterstein D., Hegamyer G., Colburn N.H.;					
RT	"Sequence and localization of a novel FK506-binding protein to mouse					
RL	chromosome 11.";					
RL	Genomics 18:407-409(1993).					
RN	[2]					
RP	SEQUENCE FROM N.A., AND CHARACTERIZATION.					
RX	MEDLINE=96094328; PubMed=7493967;					
RA	Coss M.C., Winterstein D., Sowder R.C. II, Simek S.L.;					
RT	"Molecular cloning, DNA sequence analysis, and biochemical					
RT	characterization of a novel 65-kDa FK506-binding protein (FKBP65).";					
RL	J. Biol. Chem. 270:29336-29341(1995).					
CC	-!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS DURING					
CC	PROTEIN SYNTHESIS.					
CC	-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC					
CC	PEPTIDE BONDS IN OLIGOPEPTIDES.					
CC	-!- ENZYME REGULATION: INHIBITED BY BOTH FK506 AND RAPAMYCIN, BUT NOT					
CC	BY CYCLOSPORINE A.					
CC	-!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM (POTENTIAL).					
CC	-!- TISSUE SPECIFICITY: EXPRESSED IN THE LUNG, SPLEEN, HEART, BRAIN					
CC	AND TESTIS.					
CC	-!- PTM: GLYCOSYLATED AND PHOSPHORYLATED.					
CC	-!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS 4					
CC	FKBP-LIKE DOMAINS.					
CC	-!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.					
CC	-----					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration					
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CC	the European Bioinformatics Institute. There are no restrictions on its					
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CC	or send an email to license@sib-sib.ch).					
CC	-----					
CC	EMBL; L07063; AAC37678.1; --					
DR	HSSP; P20081; 1YAT.					
DR	MGD; MGI:104769; Fkbp6.					
DR	InterPro; IPR002048; EF-hand.					

```
DR InterPro; IPR000886; ER target.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00036; ehand; 2.
DR Pfam; PF00254; FKBP; 4.
DR SMART; SM00054; Eph; 2.
DR PROSITE; PS00453; FKBP_PPIASE 1; FALSE_NEG.
DR PROSITE; PS00454; FKBP_PPIASE 2; 1.
DR PROSITE; PS00059; FKBP_PPIASE 3; 4.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00018; EF_HAND; 1.
KW Isomerase; Rotamase; Repeat; Glycoprotein; Signal; Phosphorylation;
KW Endoplasmic reticulum; Calcium-binding.
FT SIGNAL 1 33 POTENTIAL.
FT CHAIN 34 581 65 KDA FK506-BINDING PROTEIN (POTENTIAL).
FT DOMAIN 54 146 PPIASE, FKBP-TYPE 1.
FT DOMAIN 179 258 PPIASE, FKBP-TYPE 2.
FT DOMAIN 291 370 PPIASE, FKBP-TYPE 3.
FT DOMAIN 389 482 PPIASE, FKBP-TYPE 4.
FT CA_BIND 509 520 EF-HAND 2 (POTENTIAL).
FT CA_BIND 554 565 EF-HAND 2 (POTENTIAL).
FT CARBOHYD 69 69 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 181 181 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 309 309 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 351 351 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC... ) (POTENTIAL).
FT SITE 578 581 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 581 AA; 64669 MW; 1B51B302089F555 CRC64;

Query Match 57.3%; Score 1750.5; DB 1; Length 581;
Best Local Similarity 58.9%; Pred. No. 3.8e-119;
Matches 333; Conservative 90; Mismatches 131; Indels 11; Gaps 7;

QY 12 PLILLLLLV---TQAAPVAGLSGDAELQIERFVDECPRTVRSQDFVRYHYVTFPPDQ 68
Db 18 PLILLLLQTLERGLGRASP-AGAPLE-DVVIERHYIPRACPREVQMGDFVRYHYNGTFEDG 75

QY 69 QKFDSSYDRDSTFNVFVGKGLITGMDQALVGMCVNERPVKIPPKLAYGNERSGVIPP 128
Db 76 KFFDSYDSTLVAIVVGVRLITGMDRGLMGMCVNERRLVPPHLYGSGVAGLIPP 135

QY 129 NSVLHPDLVLMIDWNSDQVQIHTYFKPPSCPTIQVDFVRYHYNGTFDGLDGLFDSHSHN 188
Db 136 DATLYDFVLLVDMNKADTVQSTILLRPPYCPRMVQNSDFVRYHYNGTFDGLDGLFDSHSHN 195

QY 189 RMKTYDTYVIGWILPGMDKGLLGMCVGEKRIITIPFLAYGEDGDKDIPGOASLVFDV 248
Db 196 RGTYDTYVIGWILPGMDKGLLGMCVGEKRIITIPFLAYGEDGDKDIPGOASLVFDV 255

QY 249 ALLDLHNPXDSISIEKNVVPENCERISQSGDFTLYHYNGTLDGLTFLDSSYSRRTFDY 308
Db 256 LLLDVHNPXDTVQLETLFELPQGVRAVAGDFRYHYNGSLMDGLTFLDSSYSRRTFTY 315

QY 309 IQGVVPIGMDGLGVCIGTEKRXIIVPHLGYGEGRGN-IPGSALVFDIHDVDFHNP 367
Db 316 VQGVYIIPGMDGLOQACIGERRRITVPPLHLAGENGATGKIPGSALVFDVHDFHNP 375

QY 368 SDSISITSHYKPD-CVLSKGGDYLKHYNASLLDGLTLDSTWNLGKTYNIVLGSQGVV 426
Db 376 SDPVKILSRPEPNCNETSKIGDFIRHYNCSLLDGLTFLFSSHDEYAPQEITLGANKVI 435

QY 427 LGMDMLREMCVGEKRTVIIPHLGYGEAGVDEVPGSALVFDIEXLELVAGLPGGYMF 486
Db 436 EGLDRGLQMGCGERRQLIVPPLHLAGENGARG-VPGSALVLEFEVLVSREDGLPTGYLF 494

QY 487 IWNCEVSNLPEEIDKNGEVLLEEFSEYIIHQVASHGKGLAPGPDABELIVKMNFTNQD 546
Db 495 VVYQDPSTLFDMDLNKDGVEPPPEFSSFIKAQVNEGKRLMPGQDPDKTISDMFQND 554

QY 547 RNGDGKVTAEKFL---XDOEAKHD 568
Db 555 RNQDGKVTAEELKLKASDEDEQERVHE 579
```

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RESULT 2
FKB7 WHEAT STANDARD; PRT; 559 AA.
ID Q43207;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 70 kDa peptidylprolyl isomerase (EC 5.2.1.8) (Peptidylprolyl cis-trans
isomerase) (Cyclophilin) (PPIase).
GN FKBP70.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. ATIR; TISSUE=Root tip;
RA Oshra B., Breiman A.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PPIASE THAT BINDS CALMODULIN
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- INDUCTION: BY HEAT SHOCK.
CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS 3
FKBP-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 3 TPR REPEATS.
CC -----
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CC -----
DR EMBL; X86903; CAA60505.1; -.
DR HSSP; P27124; 1ROT.
DR InterPro; IPR001179; FKBP_PPIase.
DR InterPro; IPR001440; TPR.
DR Pfam; PF00254; FKBP; 3.
DR Pfam; PF00515; TPR; 3.
DR SMART; SM00028; TPR; 3.
DR PROSITE; PS00453; FKBP_PPIASE 1; 1.
DR PROSITE; PS00454; FKBP_PPIASE 2; 3.
DR PROSITE; PS00059; FKBP_PPIASE 3; 3.
KW Isomerase; Rotamase; Repeat; TPR repeat; Heat shock;
KW Calmodulin-binding.
FT DOMAIN 60 148 PPIASE, FKBP-TYPE 1.
FT DOMAIN 176 265 PPIASE, FKBP-TYPE 2.
FT DOMAIN 293 384 PPIASE, FKBP-TYPE 3.
FT REPEAT 401 434 TPR 1.
FT REPEAT 450 483 TPR 2.
FT REPEAT 484 517 TPR 3.
SQ SEQUENCE 559 AA; 62056 MW; 5C5DAE70D716B541 CRC64;

Query Match 12.5%; Score 382; DB 1; Length 559;
Best Local Similarity 30.1%; Pred. No. 3e-20;
Matches 113; Conservative 54; Mismatches 166; Indels 42; Gaps 11;

QY 50 TVRSQDFVRYHYVGTTFDQKFDSSYDRDSTFNVFVGKGLITGMDQALVGMCVNERFV 109
Db 56 TPBVGEVVEHYVGTTLDDGKFKDSRDRDTPFKLGGQGVKGGWQGIKTKKGENALF 115

QY 110 KIPPKLAYGNERSGVIPNSVLHFDVLLMDIWNSEDQVQIHTYFKP-----PSC 159
Db 116 TTPPELAYGESGPPPIPANATLQFVLLSUTSVRDIADKDGKIFKILKEGDKWENPKD 175

QY 160 PRTIQVSDFVRHYNGTFLDGLTFLDSSHNRMTYDTYVIGWILPGMDKGLLGMCVGEKR 219
Db 176 P-----DEVFVKYEARLEDGTVVSKSEG----VEFTVKDGHLCPALAKAVKTMKGEKV 225
```

QY 220 IITIPPFLAYGE-----DCGDKDIPGQASLVFVALLD---LHNPDKSISTENKVP--B 269
 DB 226 LIAVKFOYGFGEGRPAAGGAVPPNASVLDLWSVKTVTEIGDDKKILKVLKXEXE 285
 QY 270 NCRISQSGDFLYHYNGTLLDGLTF--DSSYSRNRTPDTYIGQYVWIPGMDGLLVCIG 328
 DB 286 GYERPNE-GAVTVTKITKLGQDTVFLKKGHDQEPFETDEAVIEGLDRAVLNKKKG 344
 QY 329 EKRXIVVPHLGYGE-EGRGN--IPGSAVLVFDIHVIDFNPSDSISITSH-----YK 378
 DB 345 EVALVTIPPEYAYGTESTEKQDAIVPPNSTVIYVELVSFVKDKESWDLNNSKTEAAGTK 404
 QY 379 PDCSVLSKKGDKLK 393
 DB 405 KEEGNALFKSGKYAR 419

RESULT 3

FKB2 MOUSE
 ID FKB2 MOUSE STANDARD; PRT; 140 AA.
 AC P45878;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE FK506-binding protein precursor (FKBP-13) (Peptidyl-prolyl cis-trans isomerase) (PPIase) (EC 5.2.1.8).
 GN FKB2 OR FKB13.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ; TISSUE=Liver;
 RX MEDLINE=94085790; PubMed=7505249;
 RA Hendrickson B.A.; Zhang W.; Craig R.J.; Jin Y.J.; Bierer R.E.; Burakoff S.J.; Dilella A.G.;
 RT "Structural organization of the genes encoding human and murine FK506-binding protein (FKBP) 13 and comparison to FKBP1.";
 RL Gene 134:271-275(1993).
 CC -!- FUNCTION: PPIases accelerate the folding of proteins. May function as a component of membrane cytoskeletal scaffolds.
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -!- ENZYME REGULATION: INHIBITED BY BOTH FK506 AND RAPAMYCIN.
 CC -!- SUBUNIT: Interacts with the C-terminal domain of 4.1G.
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN. MEMBRANE ASSOCIATED (PROBABLE).
 CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
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 CC
 CC EMBL; M77831; AAA37631.1; -
 CC HSP; P20081; 1YAT.
 CC MGD; MG1:95542; FKBP2.
 CC InterPro; IPR001179; FKBP_PPIase.
 CC Pfam; PF00254; FKBP; 1.
 CC PROSITE; PS00453; FKBP_PPIASE 1; 1.
 CC PROSITE; PS00454; FKBP_PPIASE 2; 1.
 CC PROSITE; PS00059; FKBP_PPIASE 3; 1.
 CC Isomerase; Rotamase; Signal; Endoplasmic reticulum.
 KW SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 140 FK506-BINDING PROTEIN.
 FT SITE 137 140 PREVENT SECRETION FROM ER (POTENTIAL).
 SQ SEQUENCE 140 AA; 15344 MW; F4E7FCC7766A0416 CRC64;

Query Match

Best Local Similarity 34.3%; Score 246; DB 1; Length 140;
 Matches 59; Conservative 25; Mismatches 52; Indels 36; Gaps 5;

QY 199 IGMVPGMDKGLGMCVGEKRIITPPFLAYGEDGDKDIPGQASLVFVALLDHNPKD 258
 DB 3 LSWILT-----ILSICLSA-----LAAATGAEGK-----RKL 29
 QY 259 SISTENKVVPCERISQSDELTYHYNGTLLDGLTFDSSYSRNRTPDTYIGQYVPGM 318
 DB 30 QIGVKRY--DHCPTKSRKGDVHLHMYTKLEDGTEFSSLPQNPQFVSLGTGQVIKGW 87
 QY 319 DEGLGVCIGKRXIIVPPHLYGGEGR--GNIPGSAVLVFDIHVIDFNHPSD 369
 DB 88 DQGLLGMCGEGRKLVIPSELGYGERGAPPKIPGGATLVFEVELLKIERSE 139

RESULT 4

FKB2 YEAST
 ID FKB2 YEAST STANDARD; PRT; 135 AA.
 AC P32472;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE FK506-binding protein precursor (FKBP-13) (FKBP-15) (Peptidyl-prolyl cis-trans isomerase) (PPIase) (EC 5.2.1.8).
 GN FPR2 OR FKB2 OR YDR519W OR D9719.24.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93070605; PubMed=1279908;
 RA Partridge J.A.; Fleming M.A.; Harding M.W.; Berlin V.;
 RT "Saccharomycetes cerevisiae contains a homolog of human FKBP-13, a membrane-associated FK506/zapamycin binding protein.";
 RL Yeast 8:673-680(1992).
 CC [2]
 CC SEQUENCE FROM N.A., AND SEQUENCE OF 18-54.
 CC MEDLINE=92366483; PubMed=1380159;
 CC Nielsen J.B.; Poor F.; Siekerka J.J.; Hsu M.J.; Ramadan N.;
 CC Morin N.; Shafiee A.; Dahl A.; Brizuela L.; Chretien G.;
 CC Boastian K.A.; Parent S.A.;
 CC "Yeast FKBP-13 is a membrane-associated FK506-binding protein encoded by the nonessential gene FKB2.";
 CC Proc. Natl. Acad. Sci. U.S.A. 89:7471-7475(1992).
 CC [3]
 CC SEQUENCE FROM N.A.
 CC Dietrich F.S.; Mulligan J.; Allen E.; Araujo R.; Aviles E.;
 CC Berno A.; Carpenter J.; Chen E.; Cherry J.M.; Chung E.; Duncan M.;
 CC Hunnicke-Smith S.; Hyman R.; Komp C.; Lashkari D.; Lew H.; Lin D.;
 CC Mosedale D.; Nakahara K.; Namath A.; Oefner P.; Oh C.; Petel F.X.;
 CC Roberts D.; Schramm S.; Schroeder M.; Shogren T.; Shroff N.;
 CC Winant A.; Yelton M.; Botstein D.; Davis R.W.;
 CC Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS. FKBP-13 MAY PLAY A ROLE IN PROTEIN TRAFFICKING IN THE ER.
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -!- ENZYME REGULATION: INHIBITED BY BOTH FK506 AND RAPAMYCIN.
 CC BINDS FK506 WITH 15-FOLD LOWER AFFINITY THAN FKB1.
 CC -!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. IS NOT SECRETED AND PROBABLY LOCALIZED IN THE ENDOPLASMIC RETICULUM.
 CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
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CC -----
DR EMBL; M30646; AAA34604.1; -
DR EMBL; M30767; AAA34605.1; -
DR EMBL; U33057; AAB64960.1; -
DR FIR; S25337; S25337.
DR PIR; A46154; A46154.
DR HSSP; P20081; 1YAT.
DR SGD; S0002927; FKBP2.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00254; FKBP; 1.
DR PROSITE; PS00453; FKBP_PPIASE 1; 1.
DR PROSITE; PS00454; FKBP_PPIASE 2; 1.
DR PROSITE; PS00509; FKBP_PPIASE 3; 1.
KW Isomerase; Rotamase; Signal; Endoplasmic reticulum.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 135 FK506-BINDING PROTEIN.
SQ SEQUENCE 135 AA; 14487 MW; 09CA3F1568D7E4B4 CRC64;

Query Match 8.0%; Score 244.5; DB 1; Length 135;
Best Local Similarity 43.3%; Pred. No. 4.4e-11;
Matches 55; Conservative 21; Mismatches 50; Indels 1; Gaps 1;

QY 16 LLLVWTGQAPVAGLSDAELQIERRVDPDECRPTVRSQDFVRYHYGT-FPDGQKFDSS 74
Db 5 IYLFVTFSTILAGSLSDLEIGIKRIPVEDCLIKAMPKDKVKVHYTGSLLSGTDFSS 64

QY 75 YDRDSTFNVFGVGLITGMQDALVGMVNERRFVKIPPKLAYGNERSVGVIPNSVLHF 134
Db 65 YRSGSPIAFELGVRVKGWDQVAGMCGVGEKKRLQIPSSLAYGERVPGVIPPASDLVF 124

QY 135 DVLMLDI 141
Db 125 DVELVDV 131

RESULT 5
FK21 NEUCR
ID FK21 NEUCR STANDARD; PRT; 217 AA.
AC O60046;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE FK506-binding protein precursor (FKBP-21) (Peptidyl-prolyl cis-
trans isomerase) (PPIase) (EC 5.2.1.8).
GN FKBP-21.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=74-OR23-1A;
RA Soleschield B., Tropisch M.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (Potential).
CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
CC -----
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CC -----
DR EMBL; J006297; CAA06962.1; -
DR HSSP; QJ0688; 1PBK.
DR InterPro; IPR000886; ER target.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00254; FKBP; 1.
DR -----
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DR PROSITE; PS00453; FKBP_PPIASE 1; FALSE_NEG.
DR PROSITE; PS00454; FKBP_PPIASE 2; 1.
DR PROSITE; PS00509; FKBP_PPIASE 3; 1.
DR PROSITE; PS00014; ER TARGET; 1.
KW Isomerase; Rotamase; Signal; Endoplasmic reticulum; Multigene family.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 217 FK506-BINDING PROTEIN.
FT SITE 214 217 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 217 AA; 22915 MW; 72313067521BCDAF CRC64;

Query Match 7.7%; Score 234.5; DB 1; Length 217;
Best Local Similarity 46.4%; Pred. No. 4.2e-10;
Matches 45; Conservative 15; Mismatches 36; Indels 1; Gaps 1;

QY 267 VPENCERISQSGDFTLVHYNGTL-LDGLTFDSSYSRNRFTDTYIGQYVPGMDEGLGV 325
Db 30 VPVECDRKRTRGDKINHYRGTQLSQNGQQFDASDYGRTGTFSPFKLGGGVKMGWDEGLVDM 89

QY 326 CIGEKXIVVPHLYGCEGEGNIPGSALVFDHVI 362
Db 90 CIGEKRTLTVPPSYGYGQSGIPAGSTLIFETELI 126

RESULT 6
FKB2 HUMAN
ID FKB2 HUMAN STANDARD; PRT; 141 AA.
AC P26885;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE FK506-binding protein precursor (FKBP-13) (Peptidyl-prolyl cis-trans
isomerase) (PPIase) (EC 5.2.1.8).
GN FKB2 OR FKBP13.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon carcinoma;
RC MEDLINE=91319747; PubMed=1713687;
RA Jin Y.-J., Albers M.W., Lane W.S., Bierter B.E., Schreiber S.L.,
RA Burakoff S.J.;
RT "Molecular cloning of a membrane-associated human FK506- and
rapamycin-binding protein, FKBP-13."
RT Proc. Natl. Acad. Sci. U.S.A. 88:6677-6681 (1991).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=93112052; PubMed=1281998;
RA Dilella A.G., Hawkins A., Craig R.J., Schreiber S.L., Griffin C.A.;
RT "Chromosomal band assignments of the genes encoding human FKBP12 and
FKBP13."
RL Biochem. Biophys. Res. Commun. 189:819-823 (1992).
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- ENZYME REGULATION: INHIBITED BY BOTH FK506 AND RAPAMYCIN.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN. MEMBRANE
ASSOCIATED (PROBABLE).
CC -!- TISSUE SPECIFICITY: T-CELLS AND THYMUS.
CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
CC -----
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CC -----
DR EMBL; M65128; AAA58473.1; -
DR EMBL; M75099; AAA36563.1; -
DR PIR; JCI365; JCI365.
DR -----
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RX MEDLINE=92147620; PubMed=1371107;
RA Yem A.W., Tomaselli A.G., Heinrikson R.L., Zurcher-Neely H.,
RA Ruff V.A., Johnson R.A., Deibel M.R. Jr.; complexes binds to
RT "The Hsp56 component of steroid receptor complexes binds to
RT immobilized FK506 and shows homology to FKBP-12 and FKBP-13.";
RL J. Biol. Chem. 267:2868-2871(1992).
CC -!- FUNCTION: Component of unactivated mammalian steroid receptor
CC complexes that sediment at 8-10 S. May have a rotamase activity.
CC May play a role in the intracellular trafficking of hetero-
CC oligomeric forms of steroid hormone receptors.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SUBUNIT: Associates with HSP90 and HSP70 in unactivated steroid
CC hormone receptor complexes. Also interacts with peroxisomal
CC phytenoyl-coA alpha-hydroxylase (PHYH).
CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED.
CC -!- PTM: Phosphorylation by CK2 results in loss of HSP90 binding
CC activity (By similarity).
CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
CC -!- SIMILARITY: CONTAINS 2 FKBP-TYPE PPIASE DOMAINS.
CC -!- SIMILARITY: CONTAINS 3 TPR REPEATS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M88279; AAA3611.1; -
CC EMBL; BC001786; AAH01786.1; -
CC EMBL; BC002887; AAH02887.1; -
CC EMBL; BC007924; AAH07924.1; -
CC PIR; A46372; A46372.
CC HSP; P27124; IROT.
CC Genew; HGNC:3720; FKBP4.
CC MIM; 600611; -
CC InterPro; IPR001179; FKBP_PPIase.
CC InterPro; IPR001440; TPR.
CC Pfam; PF00254; FKBP; 2.
CC Pfam; PF00515; TPR; 3.
CC SMART; SM00028; TPR; 3.
CC PROSITE; PS00453; FKBP_PPIASE 1; 1.
CC PROSITE; PS00454; FKBP_PPIASE 2; 2.
CC PROSITE; PS00059; FKBP_PPIASE 3; 2.
CC Isomerase; Rotamase; Repeat; TPR repeat; Nuclear protein;
KW Phosphorylation.
FT INIT MET 0
FT DOMAIN 49 137 PPIASE, FKBP-TYPE 1.
FT DOMAIN 166 252 PPIASE, FKBP-TYPE 2.
FT REPEAT 269 302 TPR 1.
FT REPEAT 318 351 TPR 2.
FT REPEAT 353 385 TPR 3.
FT MOD_RES 142 142 PHOSPHORYLATION (BY CK2) (BY SIMILARITY).
FT CONFLICT 145 146 ED -> AR (IN REF. 2; AAH02887).
FT SEQUENCE 458 AA; 51673 MW; 916B3B945C51634E CRC64;
Query Match 7.5%; Score 228; DB 1; Length 458;
Best Local Similarity 29.7%; Pred. No. 3.2e-09;
Matches 83; Conservative 35; Mismatches 115; Indels 46; Gaps 10;
QY 23 QAAPVAGLGDAELQ-----IERRFVDECRPTVRSGDFVRHYVGFPPDQKEDSS 74
Db 13 QSAPLPMGEVDISPKQDGLVKIKREGTGTGEMPMI---GDRVFVHYTGWLLDGTGKFDSS 69
QY 75 YDRDSTNVFVGKGLITGMDALVGMVNERFRFKIPPKLAYGNRVSQVPPNSVLHF 134
Db 70 LDRKDKFSFDLGRKEVIAKWDIAIATMKVGEVCHITCKPEYAYSAGSPKIPNATLVF 129
QY 135 DVLIM-----DIMNSED-----QVQIHTYKPPSCPTTIQVDFVRYHYNGVTFLDGTL 182

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Db 130 EVELFEPKGBDLTEEDGGIIRIQTGEGYAKP-----NEGAIVEVALEGYKDKL 181
QY 183 FDSHNMKTYDYTVYGIGW---LIPGMDKGLGMCGVEKRIITIPPLAYGDDGDK-DI 238
Db 182 FDQRELAF-----IGEGENLDLPYGLERAIQRMKEGHSIVYLKPSVAFSGVGEKFKQI 236
QY 239 PGQASLVDFVALLDLHNPKDSISIKNVKVPENCERISQS 277
Db 237 PPNAELKYELHLKSEFKAKESWEMNSE-----EKLEQS 269

RESULT 10
FKBP4_MOUSE
ID FKBP4_MOUSE STANDARD; PRT; 457 AA.
AC P30416;
DT 01-APR-1993 (Rel. 25, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE FK506-binding protein 4 (Possible peptidyl-prolyl cis-trans isomerase
DE FKBP4) (EC 5.2.1.8) (PPIase) (Rotamase) (p59 protein) (HSP binding
DE immunophilin) (HBI) (FKBP52 protein) (52 kDa FK506 binding protein)
DE (FKBP59).
GN FKBP4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=94040772; PubMed=7693550;
RA Schmitt J., Stunnenberg H.G.;
RT "Cloning and expression of a mouse cDNA encoding p59, an immunophilin
RL Gene 132:267-271(1993).
RP [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung tumor;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 5-457 FROM N.A., PARTIAL SEQUENCE, FUNCTION, AND
RP SUBCELLULAR LOCATION.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=93342084; PubMed=8341706;
RA Alnemri E.S., Fernandes-Alnemri T., Nelki D.S., Dudley K.,
RA Dubois G.C., Litwack G.;
RT "Overexpression, characterization, and purification of a recombinant
RT mouse immunophilin FKBP-52 and identification of an associated
RT phosphoprotein.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:6839-6843(1993).
CC -!- FUNCTION: Component of unactivated mammalian steroid receptor
CC complexes that sediment at 8-10 S. May have a rotamase activity.
CC May play a role in the intracellular trafficking of hetero-
CC oligomeric forms of steroid hormone receptors.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SUBUNIT: Associates with HSP90 and HSP70 in unactivated steroid
CC hormone receptor complexes. Also interacts with peroxisomal
CC phytenoyl-coA alpha-hydroxylase (PHYH) (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
CC -!- PTM: Phosphorylation by CK2 results in loss of HSP90 binding
CC activity (By similarity).
CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
CC -!- SIMILARITY: CONTAINS 2 FKBP-TYPE PPIASE DOMAINS.
CC -!- SIMILARITY: CONTAINS 3 TPR REPEATS.
CC
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CC

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Query Match

RX MEDLINE=91126049; PubMed=1704127;
 RA Wiederrecht G.J.; Brizuela L., Elliston K.O., Sigal N.H.,
 RA Stekler J.J.;
 RT "FKBP encodes a nonessential FK 506-binding protein in Saccharomyces
 cerevisiae and contains regions suggesting homology to the
 cyclophilins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:1029-1033 (1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91156723; PubMed=1705713;
 RA Heitman J., Movva R.N., Hiestand P.C., Hall M.N.;
 RT "FK 506-binding protein rotamase is a target for the
 immunosuppressive agent FK 506 in Saccharomyces cerevisiae";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:1948-1952 (1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91141524; PubMed=1996117;
 RA Koltin Y., Faucette L., Bergema D.J., Levy M.A., Cafferkey R.,
 RA Koser P.L., Johnson R.K., Livi G.P.;
 RT "Rapamycin sensitivity in Saccharomyces cerevisiae is mediated by a
 peptidyl-prolyl cis-trans isomerase related to human FK506-binding
 protein.";
 RL Mol. Cell. Biol. 11:1718-1723 (1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX STRAIN=S288c;
 RA Mallet L., Bussereau F., Jacquet M.;
 RT "A 43.5 kb segment of yeast chromosome XIV, which contains MFA2,
 MFA2, CAP/SRV2, NAM9, FKBP1/FRP1, MOM22 and CPT1, predicts an
 adenosine deaminase gene and 14 new open reading frames.";
 RL Yeast 11:1195-1209 (1995).
 RN [5]
 RP SEQUENCE OF 67-100.
 RX MEDLINE=91065908; PubMed=1701173;
 RA Stekler J.J., Widerrecht G., Greulich H., Boulton D., Hung S.H.Y.,
 RA Cryan J., Hodges P.J., Sigal N.H.;
 RT "The cytosolic-binding protein for the immunosuppressant FK-506 is
 both a ubiquitous and highly conserved peptidyl-prolyl cis-trans
 isomerase.";
 RL J. Biol. Chem. 265:21011-21015 (1990).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=93216714; PubMed=7681823;
 RA Roconda J., Burbaum J.J., Chan H.K., Marcy A.I., Becker J.W.;
 RT "Improved calcineurin inhibition by yeast FKBP12-drug complexes.
 Crystallographic and functional analysis.";
 RL J. Biol. Chem. 268:7607-7609 (1993).
 CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- MISCELLANEOUS: FKBP BINDS TO THE IMMUNOSUPPRESSANT DRUG FK506 AND
 ALSO MEDIATES THE SENSITIVITY TO RAPAMYCIN.
 CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
 CC
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 CC
 DR EMBL; Z46843; CAA86890.1; -;
 DR EMBL; M57967; AAA03564.1; -;
 DR EMBL; M60877; AAA34607.1; -;
 DR EMBL; M63892; AAA34962.1; -;
 DR EMBL; Z71411; CAA96017.1; -;
 DR PIR; A33146; A33146.
 DR PIR; A37870; A37870.
 DR PIR; A39122; A39122.
 DR PIR; C38333; C38333.

DR PIR; S13758; S13758.
 DR DB; 1YAT; 31-OCT-93.
 DR SGD; S0005079; FPR1.
 DR DR InterPro; IPR001179; FKBP_PPIase.
 DR Pfam; PF00254; FKBP; 1.
 DR PROSITE; PS00453; FKBP_PPIASE_1; 1.
 DR PROSITE; PS00454; FKBP_PPIASE_2; 1.
 DR PROSITE; PS00059; FKBP_PPIASE_3; 1.
 KW Isomerase; Rotamase; 3D-structure.
 FT STRAND 3 4
 FT HELIX 6 8
 FT STRAND 10 15
 FT TURN 25 26
 FT STRAND 28 37
 FT TURN 38 39
 FT STRAND 42 45
 FT TURN 47 50
 FT STRAND 53 56
 FT TURN 57 58
 FT HELIX 64 72
 FT TURN 75 76
 FT STRAND 78 83
 FT HELIX 85 87
 FT TURN 88 92
 FT STRAND 94 94
 FT TURN 95 97
 FT STRAND 98 98
 FT TURN 100 101
 FT STRAND 104 113
 SQ SEQUENCE 114 AA; 65C134830D30C06 CRC64;
 12158 MW; 65C134830D30C06 CRC64;
 Query Match 6.8%; Score 207; DB 1; Length 114;
 Best Local Similarity 43.8%; Pred. No. 1.8e-08;
 Matches 44; Conservative 13; Mismatches 44; Indels 0; Gaps 0;
 QY 41 RFVDECPRTVRSQDFVRYHYVGFDPGQKQFDSYDSTFNFGKQLITGMDQALVG 100
 Db 13 RISPGDGTGPKGDLVTIHYTGLENGKFDSDVDRGSPQCNGVGVKIGWDVGPK 72
 QY 101 MCVNERFVKIPKLAAYGNVRSVIPPNSVLHFDVLMDI 141
 Db 73 LSVGEKARLTIPGYAYGPRGPGIIPNSTLVDFVLLKV 113
 RESULT 14
 FKBP_SCHPO
 ID _FKBP_SCHPO STANDARD; PRT; 112 AA.
 AC Q42993;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE FK506-binding protein (FKBP) (Peptidyl-prolyl cis-trans isomerase)
 DE (PPIase) (EC 5.2.1.8).
 GN SPC24E9.17C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=91848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgourou J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

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RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckart G., Aert R., Robben J., Grymonprez B.,
RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritsch C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Rhode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., Del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS (BY
CC SIMILARITY).
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- MISCELLANEOUS: FKBP BINDS TO THE IMMUNOSUPPRESSANT DRUG FK506.
CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
CC -----
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CC -----
DR EMBL; AL096796; CAB46710.1; -
DR HSSP; P20081; IYAT.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00254; FKBP; 1.
DR PROSITE; PS00453; FKBP_PPIASE_1; 1.
DR PROSITE; PS00454; FKBP_PPIASE_2; 1.
DR PROSITE; PS50059; FKBP_PPIASE_3; 1.
KW Isomerase; Rotamase.
SQ SEQUENCE 112 AA; 12043 MW; 355944ECB84D2539 CRC64;

Query Match 6.4%; Score 196; DB 1; Length 112;
Best Local Similarity 45.6%; Pred. No. 1.1e-07;
Matches 41; Conservative 12; Mismatches 37; Indels 0; Gaps 0;

QY 52 RSGDFVRYHYVCTPFGQKFDSSYDRDSTFNVFVGKGLITGMQALVGMCVNRRFVKI 111
DB 18 KPGDRITMHTYGTLTNGKKFDSSYDRGSPFVCTTIGVQGLIRGWDGVPKMSLGEKAKLTI 77

QY 112 PPKLAYGNVRSVGIIPNLSVLHFDVLLMDI 141
DB 78 TPDYGYGPRGPFGLIPNSTLLFDVLLAI 107

RESULT 15
FKBL DROME
ID FKBL DROME STANDARD; PRT; 108 AA.
AC P48375;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 12 kDa FK506-binding protein (FKBP) (Peptidyl-prolyl cis-trans
DE isomerase) (PPIase) (EC 5.2.1.8) (Macrolide binding protein).
GN FK506-BP2 OR FKBP12.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
TISSEU=Head;
STRAIN=Canton-S;

```

```

RA Mounsey A.;
RA Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RA Wang T., Li B.Y., Danielson P.D., Shah P.C., Rockwell S.,
RA Lechleider R.J., Martin J., Manganaro T., Donahoe P.K.;
RA Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RL -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
CC -----
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CC -----
DR EMBL; Z49079; CAA88904.1; -
DR EMBL; U41441; AAR91178.1; -
DR HSSP; P18203; IFKL.
DR FlyBase; FBgn0013954; FK506-bp2.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00254; FKBP; 1.
DR PROSITE; PS00453; FKBP_PPIASE_1; 1.
DR PROSITE; PS00454; FKBP_PPIASE_2; 1.
DR PROSITE; PS50059; FKBP_PPIASE_3; 1.
KW Isomerase; Rotamase.
SQ SEQUENCE 108 AA; 11597 MW; 48BCF993AC8D350A CRC64;

Query Match 6.4%; Score 195.5; DB 1; Length 108;
Best Local Similarity 36.1%; Pred. No. 1.1e-07;
Matches 43; Conservative 16; Mismatches 45; Indels 15; Gaps 1;

QY 23 QAAPVAGLGSDAELQIERRFVDECPRTVRSQGDVRYHYVGTFFDGQKFDSSYDRDSTFN 82
DB 4 QVVPIA-----FQDGSYTPKNGQKVTVHYTGTLLDGTGTFDSSRDNRKPFK 48

QY 83 VFGVKGLITGMQALVGMCVNRRFVKIPPKLAYGNVRSVGIIPNLSVLHFDVLLMDI 141
DB 49 FTIGRGEVIRGWDEGVAGLQSVQSAKLICSPDYAYGSRGHPGVIPNLSLTDFVELLKV 107

Search completed: April 26, 2003, 06:56:20
Job time : 12.2323 secs

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GenCore version 5.1.4 p5.4578
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OM protein - protein search, using sw model

Run on: April 26, 2003, 06:48:54 ; Search time 50.5014 Seconds
(without alignments)
2341.934 Million cell updates/sec

Title: US-09-225-502-6

Perfect score: 3054

Sequence: 1 MAPRGWRPPPPPLLLLLLWV.....AEEFLLXQBAKHVDVTLNLA 574

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 21:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	2805	91.8	570	11 Q8R386	Q8r386 mus musculu
2	2796	91.6	570	11 Q9Z247	Q9z247 mus musculu
3	2723	89.2	517	4 Q95302	Q95302 homo sapien
4	2380.5	77.9	577	13 Q9YIC3	Q9yic3 gallus gall
5	1772	58.0	564	13 Q9I8P8	Q9i8p8 xenopus lae
6	1753.5	57.4	581	11 Q8VHI1	Q8vhi1 mus musculu
7	1744	57.1	582	4 Q9H3N3	Q9h3n3 homo sapien
8	1742	57.0	582	4 Q96AY3	Q96ay3 homo sapien
9	1522	49.8	481	4 Q9H6N5	Q9h6n5 homo sapien
10	845.5	27.7	355	4 Q9H6J3	Q9h6j3 homo sapien
11	736	24.1	262	4 Q9UF89	Q9uf89 homo sapien
12	464.5	15.2	137	13 Q98UD7	Q98ud7 xenopus lae
13	344.5	11.3	261	5 Q16309	Q16309 caenorhabdi
14	343	11.2	264	5 P91180	P91180 caenorhabdi
15	343	11.2	300	5 Q95Q60	Q95q60 caenorhabdi
16	338.5	11.1	578	10 Q9FJL3	Q9fjl3 arabisopsis

17	311	10.2	551	10 Q38931	Q38931 arabisopsis
18	311	10.2	551	10 Q38949	Q38949 arabisopsis
19	311	10.2	555	10 Q9LSF3	Q9lsf3 arabisopsis
20	309	10.1	216	5 Q9V3V2	Q9v3v2 drosophila
21	307	10.1	216	5 Q9XZ54	Q9xz54 drosophila
22	307	10.1	568	10 Q04843	Q04843 triticum ae
23	294.5	9.6	259	5 Q23338	Q23338 caenorhabdi
24	286.5	9.4	139	5 Q20107	Q20107 caenorhabdi
25	270	8.8	138	5 Q9VGK3	Q9vgk3 drosophila
26	268	8.8	222	4 Q9Y6B0	Q9y6b0 homo sapien
27	268	8.8	222	4 Q96DA4	Q96da4 homo sapien
28	267.5	8.8	209	5 Q966Y5	Q966y5 suberites d
29	263.5	8.6	312	2 Q53919	Q53919 streptomyce
30	263	8.6	151	10 Q41649	Q41649 vicia faba
31	262.5	8.6	304	5 Q9XW05	Q9xw05 caenorhabdi
32	259.5	8.5	163	10 Q9FJL2	Q9fjl2 arabisopsis
33	259.5	8.5	163	10 Q38936	Q38936 arabisopsis
34	256	8.4	211	4 Q9NWM8	Q9nmw8 homo sapien
35	256	8.4	218	11 Q54998	Q54998 mus musculu
36	254.5	8.3	134	5 Q17280	Q17280 botryllus s
37	253.5	8.3	589	10 Q94J55	Q94j55 oryza sativ
38	253	8.3	146	10 Q38935	Q38935 arabisopsis
39	253	8.3	153	10 Q9LSF4	Q9lsf4 arabisopsis
40	249.5	8.2	259	4 Q9Y680	Q9y680 homo sapien
41	242.5	7.9	142	4 Q9BTS7	Q9bts7 homo sapien
42	231.5	7.6	137	5 Q96335	Q96335 brugia mala
43	226	7.4	439	5 Q9U4N1	Q9u4n1 drosophila
44	225.5	7.4	152	5 Q8T109	Q8t109 bombyx mori
45	225	7.4	439	5 Q9VL78	Q9vl78 drosophila

ALIGNMENTS

RESULT 1

Q8R386

ID Q8R386 PRELIMINARY; PRT; 570 AA.

AC Q8R386; (TREMBLrel. 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE FK506 binding protein 9.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Strausberg R.;

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC026133; AAH26133.1; --

SQ SEQUENCE 570 AA; 63014 MW; 06AB7BD18786B9D5 CRC64;

Query Match 91.8%; Score 2805; DB 11; Length 570;

Best Local Similarity 93.1%; Pred. No. 3.5e-215;

Matches 526; Conservative 15; Mismatches 22; Indels 2; Gaps 1;

QY	4	RGWRPPPPPLLLLLLWTGQAAPVAGLGSDAEIQIERRFVDPDECPRTVRSQDFVRYHYVG	63
DB	6	RGWR--RRSLLLLLWTGQAAPVLGLAVSSSELQIQRSFVDPDECPRTVHSGDFVRYHYVG	63
QY	64	TFPDGOKFSSYDRDSTFNFGKGLITGMDQALVGMVNERFVKIPPKLAYGNERS	123
DB	64	TFUDGOKFSSYDRDSTFNFGKGLITGMDQALVGMVNERLVTIPPMLAYSGEVS	123
QY	124	GVIPPNVLHFDVLLMDWNSEDOVQIHTYFKPSCPRTIQVDFRVYHYNGTFLDGLTFL	183
DB	124	GVIPPNVLHFDVLLMDWNSEDOVQIHTYFKPSCPRTIQVDFRVYHYNGTFLDGLTFL	183
QY	184	DSHNRMKTYDVTYVGIGWLIPGMDKGLLGMVCGEKRITITPPFLAYGEGDGKQIPGQAS	243
DB	184	DSHNRMKTYDVTYVGIGWLIPGMDKGLLGMVCGEKRITITPPFLAYGEGDGKQIPGQAS	243

QY 244 LVFDVALLDHPKDSISIKNVKVPENCERISQSGDFLTTHYNGTLLDGTDFDSSYSRNR 303
 DB 244 LVFDVALLDHPKDSISIKNVKVPENCERISQSGDFLTTHYNGTLLDGTDFDSSYSRNRH 303
 QY 304 TPTDTYIGQGVYIPQWDEGLLVCIGCEKXIXVPPHLYGEGEGRNIPGSAVLVDFDHIHVID 363
 DB 304 TPTDTYIGQGVYIPQWDEGLLVCIGCEKXIXVPPHLYGEGEGRNIPGSAVLVDFDHIHVID 363
 QY 364 FHPSPDSISITSHYKPPDCSVLSKGDYKLYHNASLDDGTLLDSTWNLGKTYNIVLGS 423
 DB 364 FHPSPDSISITSHYKPPDCSVLSKGDYKLYHNASLDDGTLLDSTWNLGKTYNIVLGS 423
 QY 424 QVVLGMDMGLRECMVCGEKRITVIIIPHLGYGAGVDGVEPGSAVLVDFDIEKLVLVAGLPRG 483
 DB 424 QVVLGMDMGLRECMVCGEKRITVIIIPHLGYGAGVDGVEPGSAVLVDFDIEKLVLVAGLPRG 483
 QY 484 YMFIMNGEVSNTLFEEDKNGEVLLEEFSEYIIHAQVATGKGLAPGFAEIVKNNMT 543
 DB 484 YMFIMNGEVSNTLFEEDKNGEVLLEEFSEYIIHAQVATGKGLAPGFAEIVKNNMT 543
 QY 544 NDRNGDGKVTAEFKLXDOEAKHD 568
 DB 544 NDRNGDGKVTAEFKLXDOEAKHD 568 36

RESULT 2
 Q92247 PRELIMINARY; PRT; 570 AA.
 AC Q92247 Q9JHX5; Q9CVM0;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE PK506 binding protein 9 precursor (EC 5.2.1.8) (Peptidyl-prolyl cis-
 trans isomerase) (PPIase) (Rotamase) (TKBP65RS).
 GN FKBP9 OR FKBP63.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., ENZYME REGULATION, SUBCELLULAR LOCATION, TISSUE
 RP SPECIFICITY, DEVELOPMENTAL STAGE, AND CALCIUM-BINDING ACTIVITY.
 RX MEDLINE=99453729; PubMed=10524204;
 RA Shadidy M., Caubit X., Olsen R., Seternes O.M., Moens U., Krause S.;
 RT "Biochemical analysis of mouse FKBP60, a novel member of the FKBP
 RT family".
 RL Biochim. Biophys. Acta 1446:295-307 (1999).
 RN [2]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RP TISSUE=THYMUS;
 RX PubMed=11710534;
 RA Jo D., Iyu M.S., Cho E.-G., Park D., Kozak C.A., Kim M.G.;
 RT "Identification and genetic mapping of the mouse Fkbp9 gene encoding a
 RT new member of FK506-binding protein family".
 RL Mol. Cells 12:272-275 (2001).
 RN [3]
 RP SEQUENCE OF 155-570 FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Kleihschmann W., Gaaslerland T., Giesi C., King B., Kochiwa H.,
 RA Kuenl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furumaki M., Aono H., Baldarelli R., Barch G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690 (2001)
 CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS DURING
 CC PROTEIN SYNTHESIS.
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -!- ENZYME REGULATION: INHIBITED BY FK506.
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
 CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN HEART, SKELETAL
 CC MUSCLE, LUNG, LIVER AND KIDNEY. LOWER LEVELS FOUND IN BRAIN,
 CC SPLEEN AND TESTIS.
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN ALL DEVELOPMENTAL STAGES.
 CC -!- PTM: PHOSPHORYLATED.
 CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS 4
 CC FKBP-LIKE DOMAINS.
 CC -!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 CC EMBL; AF090334; AAC72964.1; -;
 CC EMBL; AF279263; AAF79215.1; -;
 CC EMBL; AK007499; BAB25071.1; -;
 CC HSSP; P20081; 1YAT.
 CC MGD; MGI:1350921; Fkbp9.
 CC InterPro; IPR002048; EF-hand.
 CC InterPro; IPR000886; ER target.
 CC InterPro; IPR001179; FKBP_PPIase.
 CC Pfam; PF00036; efhand; 2.
 CC Pfam; PF00254; FKBP; 4.
 CC SMART; SM00054; Eph; 2.
 CC PROSITE; PS00018; EF_HAND; 1.
 CC PROSITE; PS00014; ER_TARGET; 1.
 CC PROSITE; PS00453; FKBP_PPIASE 1; FALSE_NEG.
 CC PROSITE; PS00454; FKBP_PPIASE 2; 3.
 CC PROSITE; PS00509; FKBP_PPIASE 3; 4.
 CC Isonerases; Rotamase; Repeat; Glycoprotein; Signal; Phosphorylation;
 KW Endoplasmic reticulum; Calcium-binding.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 570 FK506 BINDING PROTEIN 9.
 FT DOMAIN 45 139 PPIASE, FKBP-TYPE 1.
 FT DOMAIN 158 251 PPIASE, FKBP-TYPE 2.
 FT DOMAIN 269 362 PPIASE, FKBP-TYPE 3.
 FT DOMAIN 381 474 PPIASE, FKBP-TYPE 4.
 FT CA_BIND 492 520 PPIASE, FKBP-TYPE 4.
 FT SITE 537 563 EF-HAND 2 (POTENTIAL).
 FT SITE 567 570 EF-HAND 2 (POTENTIAL).
 FT CARBOHYD 174 174 PREVENT SECRETION FROM ER (POTENTIAL).
 FT CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 234 236 DGK -> NGE (IN REF. 2).
 FT CONFLICT 321 321 G -> S (IN REF. 3).
 FT CONFLICT 351 351 G -> A (IN REF. 2).
 FT CONFLICT 353 353 A -> T (IN REF. 3).
 FT CONFLICT 361 361 V -> F (IN REF. 2).
 FT CONFLICT 364 364 F -> V (IN REF. 2).
 FT CONFLICT 378 378 K -> N (IN REF. 2).
 FT CONFLICT 386 386 S -> I (IN REF. 2).
 FT CONFLICT 475 475 E -> D (IN REF. 2).
 FT CONFLICT 550 550 D -> N (IN REF. 2).
 SQ SEQUENCE 570 AA; 62995 MW; DFE8B8F2F6A0FIDA CRC64;
 Query Match 91.6%; Score 2796; DB 11; Length 570;
 Best Local Similarity 92.7%; Pred. No. 1.9e-214;
 Matches 524; Conservative 16; Mismatches 23; Indels 2; Gaps 1;
 QY 4 RGRPPPPPLLLLLLWVGQAAPVAGLSDAELQIERFVDECPRTVRSQDFFVHYVG 63
 DB 6 RGRW-RRSLLLLLWVGQAAPVGLAVSELQIQSFVDECPRTVHSQDFFVHYVG 63
 QY 64 TFPDQKGFSSYDRDSTFNVFVGKQLITGMDOALVGMVNERFVKIPPKLAYNERVS 123

Db 64 TFLDQKFDSSYDRDSTFNVFGKQLIAGMDQALVCMVNERELVTIPPNLAYSGSEGS 123
 QY 124 GVTPPNSVLHFDVLLMDIWNSEDOVQIHTYFKPPSCPRRTIQQVDFVRYHNGTFLDGTLP 183
 Db 124 GVTPPNSVLHFDVLLMDIWNSEDOVQIHTYFKPPSCPRRTIQQVDFVRYHNGTFLDGTLP 183
 QY 184 DSSHNRKMTYDVTYVGLIPLGMDKGLGMCVGEKRIITIPPLAYGEGDGKDIPOGAS 243
 Db 184 DSSHNRKMTYDVTYVGLIPLGMDKGLGMCVGEKRIITIPPLAYGEGDGKDIPOGAS 243
 QY 244 LVPDVALDLHNPKDSISIEKVVPCNERISQSGDFLTTHYNGTLLDGTFLDSSYSNR 303
 Db 244 LVPDVALDLHNPKDSISIEKVVPCNERISQSGDFLTTHYNGTLLDGTFLDSSYSNR 303
 QY 304 TPTTYIGQGVVPGMDGLGVCIGEXXIVVPPHLYGEGRGNIPOGSAVLVDFDIHVID 363
 Db 304 TPTTYIGQGVVPGMDGLGVCIGEXXIVVPPHLYGEGRGNIPOGSAVLVDFDIHVID 363
 QY 364 FHNPSDSISITSHYKPPDCSVLSKGDYLVKHYNASLLDGTLLDSTWNLTGTYNIVLGS 423
 Db 364 FHNPSDSISITSHYKPPDCSVLSKGDYLVKHYNASLLDGTLLDSTWNLTGTYNIVLGS 423
 QY 424 QVVLGMDGLREMCVGEKRTIIPPHLYGEGAGVDGVPVSAVLVDFIEXLELVAGLPEG 483
 Db 424 QVVLGMDGLREMCVGEKRTIIPPHLYGEGAGVDGVPVSAVLVDFIEXLELVAGLPEG 483
 QY 484 YMFVWGEVSPNLFEEIDKXNGEVLLEEFSEYTHAQVASKGLAPGFAELIVKQNT 543
 Db 484 YMFVWGEVSPNLFEEIDKXNGEVLLEEFSEYTHAQVASKGLAPGFAELIVKQNT 543
 QY 544 NQRNGDGKVTAEFKLDOEAKHD 568
 Db 544 NQRNGDGKVTAEFKLDOEAKHD 568
 RESULT 3
 095302 PRELIMINARY; PRT; 517 AA.
 AC 095302; 0961J9; 096EX5;
 DT 01-MAY-1999 (TREMUREl. 10, Created)
 DT 01-MAY-1999 (TREMUREl. 10, Last sequence update)
 DT 01-MAR-2002 (TREMUREl. 20, Last annotation update)
 DE FK506 binding protein 9 (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (Fragment).
 GN FKBP9 OR FKBP63.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99453729; PubMed=10524204;
 RA Shaddy M., Caubit X., Olsen R., Seternes O.M., Moens U., Krauss S.;
 RT "Biochemical analysis of mouse FKBP60, a novel member of the FKBP family";
 RL Biochim. Biophys. Acta 1446:295-307(1999).
 RN [2]
 RP SEQUENCE OF 317-517 FROM N.A.
 RC TISSUE=KIDNEY, AND MUSCLE;
 RA Strausberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS DURING PROTEIN SYNTHESIS.
 CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -1- ENZYME REGULATION: INHIBITED BY FK506 (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM (BY SIMILARITY).
 CC -1- PTM: PHOSPHORYLATED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS 4 FKBP-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 DR EMBL; AF089745; AAC78853.1; -;
 DR EMBL; BC007443; AAH07443.1; -;

DR EMBL; BC011872; AAH11872.1; -;
 DR HSPF; P20081.1; YAT
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR000886; ER target.
 DR InterPro; IPR001179; FKBP_PPIase.
 DR Pfam; PF00036; ehand; 2.
 DR Pfam; PF00254; FKBP; 4.
 DR SMART; SM00054; EFh; 2.
 DR PROSITE; PS00016; EF_HAND; 1.
 DR PROSITE; PS00014; ER_TARGET; 1.
 DR PROSITE; PS00453; FKBP_PPIASE_1; FALSE_NEG.
 DR PROSITE; PS00454; FKBP_PPIASE_2; 3.
 DR PROSITE; PS00509; FKBP_PPIASE_3; 4.
 KW Isomerase; Rotamase; Repeat; Glycoprotein; Phosphorylation;
 KW Endoplasmic reticulum; Calcium-binding.
 FT NON_TER 1 1
 FT DOMAIN 1 86 PPIASE, FKBP-TYPE 1.
 FT DOMAIN 105 198 PPIASE, FKBP-TYPE 2.
 FT DOMAIN 216 309 PPIASE, FKBP-TYPE 3.
 FT DOMAIN 328 421 PPIASE, FKBP-TYPE 4.
 FT CA_BIND 439 467 EF-HAND 1 (POTENTIAL).
 FT CA_BIND 484 510 EF-HAND 2 (POTENTIAL).
 FT SITE 514 517 PREVENT SECRETION FROM ER (POTENTIAL).
 FT CARBOHYD 121 121 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 233 233 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 249 249 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 344 344 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CONFLICT 317 319 SIS -> HEG (IN REF. 2; AAH07443).
 FT CONFLICT 514 514 H -> Q (IN REF. 2; AAH11872).
 SQ SEQUENCE 517 AA; 57219 MW; 704FBOCE9C4C74B CRC64;
 Query Match 89.2%; Score 2723; DB 4; Length 517;
 Best Local Similarity 99.0%; Pred. No. 1.1e-208;
 Matches 510; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 54 GDFVRYHYVGTFFDQKFDSSYDRDSTFNVFGKQLITGMDQALVCMVNERRFVKIPP 113
 Db 1 GDFVRYHYVGTFFDQKFDSSYDRDSTFNVFGKQLITGMDQALVCMVNERRFVKIPP 60
 QY 114 KLAYGNRVSGVVPNSVLHFDVLLMDIWNSEDOVQIHTYFKPPSCPRRTIQQVDFVRYH 173
 Db 61 KLAYGNRVSGVVPNSVLHFDVLLMDIWNSEDOVQIHTYFKPPSCPRRTIQQVDFVRYH 120
 QY 174 NGTFDGLTFLDSSHNRKMTYDVTYVGLIPLGMDKGLGMCVGEKRIITIPPLAYGEDG 233
 Db 121 NGTFDGLTFLDSSHNRKMTYDVTYVGLIPLGMDKGLGMCVGEKRIITIPPLAYGEDG 180
 QY 234 DGKDIPGQASLVFDVALLDLHNPKDSISIEKVVPCNERISQSGDFLTTHYNGTLLDGT 293
 Db 181 DGKDIPGQASLVFDVALLDLHNPKDSISIEKVVPCNERISQSGDFLTTHYNGTLLDGT 240
 QY 294 LFDSSYSNRRTFTTYIGQGVVPGMDGLGVCIGEXXIVVPPHLYGEGRGNIPOGSA 353
 Db 241 LFDSSYSNRRTFTTYIGQGVVPGMDGLGVCIGEXXIVVPPHLYGEGRGNIPOGSA 300
 QY 354 VLVFDIHVDFHNPSDSISITSHYKPPDCSVLSKGDYLVKHYNASLLDGTLLDSTWNLG 413
 Db 301 VLVFDIHVDFHNPSDSISITSHYKPPDCSVLSKGDYLVKHYNASLLDGTLLDSTWNLG 360
 QY 414 KTYNIVLGSQVVLGMDGLREMCVGEKRTIIPPHLYGEGAGVDGVPVSAVLVDFIEX 473
 Db 361 KTYNIVLGSQVVLGMDGLREMCVGEKRTIIPPHLYGEGAGVDGVPVSAVLVDFIEX 420
 QY 474 LELVAGLPGYMFVWGEVSPNLFEEIDKXNGEVLLEEFSEYTHAQVASKGLAPGPD 533
 Db 421 LELVAGLPGYMFVWGEVSPNLFEEIDKXNGEVLLEEFSEYTHAQVASKGLAPGPD 480
 QY 534 AELIVKQNTQDRNGDGKVTAEFKLDOEAKHD 568
 Db 481 AELIVKQNTQDRNGDGKVTAEFKLDOEAKHD 515
 RESULT 4

Q9YIC3

ID Q9YIC3 PRELIMINARY; PRT; 577 AA.
AC Q9YIC3
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE CFBP/SMAP.
GN CFBP/SMAP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98384310; PubMed=9716519;
FA Fukuda K., Tanigawa Y., Fujii G., Yasugi S., Hirohashi S.;
RT "CFBP/SMAP; a novel molecule involved in the regulation of smooth
muscle differentiation.";
RL Development 125:3535-3542(1998).
DR EMBL; AB008675; BAA34673.2; -.
DR HSSP; P27124; 1R0T.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000886; ER target.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00036; ehand; 2.
DR Pfam; PF00254; FKBP; 4.
DR SMART; SM00054; EPH; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
DR PROSITE; PS00454; FKBP_PPIASE_2; UNKNOWN_3.
DR PROSITE; PS00059; FKBP_PPIASE_3; 4.
SQ SEQUENCE 577 AA; 64054 MW; 1E85DEA387AE099B CRC64;

Query Match 77.9%; Score 2380.5; DB 13; Length 577;
Best Local Similarity 78.6%; Pred. No. 2.6e-181;
Matches 442; Conservative 54; Mismatches 55; Indels 11; Gaps 4;

QY 15 LLLLLWVTOAAPVAGL---GSDAELQIERFVDECPRTVRSQDFVRYHYVGFDPQKQF 71
DB 17 LLVSWAACQAPPVAAEPWGDADVHVERFVPERLPRVRRGDFVRYHYLGFDPQTRF 76
QY 72 DSSYDRDSTFNVFVGKQLITGMDQALVGMVNERFVKIPPKLAYGNERSVGVPNSV 131
DB 77 DSSYDRGSTFNVFVGKQLITGMDQALVGMVNERFVKIPPKLAYSGEGVGVPNAV 136
QY 132 LHFDVLLMDIWNSEDQVQIHTVFKPPSCPTIOVSDFVRYHYNGTFLDGTLPSSSHNRMK 191
DB 137 LHFDVLLMDIWNSEDQVQIHTVFKPPSCPTIOVSDFVRYHYNGTFLDGTLPSSSHNRMR 196
QY 192 TYDTYVIGIWLIPGMDKGLLGMVCGEKRIITIPFLAYGSDGDKDIPQASLVDFVALL 251
DB 197 TYDTYVIGIWLIPGMDKGLLGMVCGEKRIITIPFLAYGSDGDKDIPQASLVDFVALL 256
QY 252 DLHNPDSISIKNVVPCERISQSGDPLTYHYNGTFLDGTLPSSSYNRNFTDYIGQ 311
DB 257 DLHNPDKGITIENQLVPESCERRTQTQDFRHYNGTFLDGTLPSSSYNRNFTDYIGQ 316
QY 312 GVIIPGMDKGLLGMVCGEKRIITIPFLAYGSDGDKDIPQASLVDFVALL 371
DB 317 GVIIPGMDKGLLGMVCGEKRIITIPFLAYGSDGDKDIPQASLVDFVALL 376
QY 372 SITSHYKPPDCSVLKKGDYLYHYNASLTI---DGTLLDSTWNLGKTYNVLGSGQVVLG 428
DB 377 SITVNYKPCNSCLLSKKGDYLYHYNASLTI---DGTLLDSTWNLGKTYNVLGSGQVVLG 433
QY 429 MDMLREMCVGEKRTVIIPPHLYGAGVDGVEGPGSAVLVFDIEXLELVAGLPEGYMFIV 488
DB 434 MDMLQDMCVGERRTVIIPPHLYGAGVDGVEGPGSAVLVFDIEXLELVAGLPEGYMFIV 493
QY 489 NGEVSPNLFEEIDKQNGSVLLREFSEYIHAQVASCCKGLACGDAELVKNMFTNQDRN 548
DB 494 NGEVSPNLFEEIDKQNGSVLLREFSEYIHAQVASCCKGLACGDAELVKNMFTNQDRN 553

QY 549 GDGKVTAEFFKLDQAEAK--HD 568
DB 554 GNGKVTAEFFKLDQAEKEGHD 575

RESULT 5

Q918P8
ID Q918P8 PRELIMINARY; PRT; 564 AA.
AC Q918P8
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE FK506-binding protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20302564; PubMed=10842073;
FA Spokony R., Saint-Jeannet J.-P.;
RT "Xenopus FK 506-binding protein, a novel immunophilin expressed during
early development.";
RL Mech. Dev. 94:205-208(2000).
DR EMBL; AF232672; AAF35906.1; -.
DR HSSP; P20081; 1YAT.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000886; ER target.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00036; ehand; 2.
DR Pfam; PF00254; FKBP; 4.
DR SMART; SM00054; EPH; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
DR PROSITE; PS00454; FKBP_PPIASE_2; UNKNOWN_2.
DR PROSITE; PS00059; FKBP_PPIASE_3; 4.
SQ SEQUENCE 564 AA; 62643 MW; 15312365BF1B43CF CRC64;

Query Match 58.0%; Score 1772; DB 13; Length 564;
Best Local Similarity 59.5%; Pred. No. 8.5e-133;
Matches 329; Conservative 82; Mismatches 134; Indels 8; Gaps 3;

QY 13 LLLLLWVTOAAPVAGLSDAELQIERFVDECPRTVRSQDFVRYHYVGFDPQKQF 72
DB 10 LHFLVLYVACDQGL-----EDVVIDRDIPIKICPREVQMGDFVRYHYNGTFFKDGQKFD 63
QY 73 SSYDRDSTFNVFVGKQLITGMDQALVGMVNERFVKIPPKLAYGNERSVGVPNSV 132
DB 64 ASYDRGVAVAGVGVGRLITGLDRGILGMVNEKRLIVPPHLYGSGIVGPMIPADATL 123
QY 133 HFVLLMDIWNSEDQVQIHTVFKPPSCPTIOVSDFVRYHYNGTFLDGTLPSSSHNRMT 192
DB 124 YFDILLQDIWNKDEVOITTIHKASPCNRSVQSDDFVRYHYNGTFLDGTLPSSSYRSTT 183
QY 193 YDTYVIGIWLIPGMDKGLLGMVCGEKRIITIPFLAYGSDGDKDIPQASLVDFVALL 252
DB 184 YDTYVIGIWLIPGMDKGLLGMVCGEKRIITIPFLAYGSDGDKDIPQASLVDFVALL 243
QY 253 LHNPKDISIKNVVPCERISQSGDPLTYHYNGTFLDGTLPSSSYNRNFTDYIGQ 312
DB 244 FHNPKDITVQNVQVPCRRKAVIGDYRYHYNGTFLDGTLPSSSYNRNFTDYIGQ 303
QY 313 YVTPGMDKGLLGMVCGEKRIITIPFLAYGSDGDKDIPQASLVDFVALL 371
DB 304 YVTPGMDKGLLGMVCGEKRIITIPFLAYGSDGDKDIPQASLVDFVALL 363
QY 372 SITSHYKPPDCSVLKKGDYLYHYNASLTI---DGTLLDSTWNLGKTYNVLGSGQVVLG 431
DB 364 DIEVMKPDSCNTTSKKGDFIKYHNCMLDGTLLFFSHEBYETPQQVTGLGSKVIEGIDT 423
QY 432 GLREMCVGEKRTVIIPPHLYGAGVDGVEGPGSAVLVFDIEXLELVAGLPEGYMFIV 491

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Db 424 GLLCMVGERTVLPPLAHGSGARG-VPPSAVLAFDLELLHIEGIPDGYLFIWLD 482
QY 492 VSNLFEIDKNGEVLLEEFSEYIIHAQVAGSGKGLAPGDAELIVKNMFTNQDRNGD 551
Db 483 TPNELFEIMDLKNGEVPPEFSDFLKAQVSEKGRFLPGVDREKSTADMEVQDRNKG 542
QY 552 KVTAEEFKLXDOE 564
Db 543 KITADELKUKTEE 555

RESULT 6
Q8VH11 PRELIMINARY; PRT; 581 AA.
AC Q8VH11;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 65 kDa FK506-binding protein.
GN FKBP10.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Patterson C.E., Gao J., Rooney A.P., Davis E.C.;
RT "Genomic Organization of Mouse and Human 65 kDa FK506-binding protein
  (FKBP65) Genes and Evolution of the FKBP Multigene Family.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF456413; AAL57621.1; JOINED.
DR EMBL; AF456412; AAL57621.1; JOINED.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000886; ER target.
DR InterPro; IPR001179; FKBP_PPase.
DR Pfam; PF00036; ehand; 2.
DR Pfam; PF00254; FKBP; 4.
DR SMART; SM00054; EFh; 2.
DR PROSITE; PS00018; EF HAND; UNKNOWN 1.
DR PROSITE; PS00014; ER TARGET; UNKNOWN 1.
DR PROSITE; PS00454; FKBP_PPASE 2; UNKNOWN 1.
DR PROSITE; PS00059; FKBP_PPASE 3; 4.
SQ SEQUENCE 581 AA; 64697 MW; FD6F777940AD91B9 CRC64;

Query Match 57.4%; Score 1753.5; DB 11; Length 581;
Best Local Similarity 58.9%; Pred. No. 2.6e-131;
Matches 333; Conservative 90; Mismatches 131; Indels 11; Gaps 7;

QY 12 PLILLILLWV---TQAPAVAGLSDAELOIERFVDPDPCRTVRSGLDVRHYHVTFFDG 68
Db 18 PLILLQLTERGLGRASP-AGAPLE-DVIERHYHIPRACPREVQMGDFVRYHYNGTFDG 75
QY 69 OKPDSSYDRSTFNVFVGKGLITGMDOALVGMCVNERFVKIPKLAGNERVSGVIPP 128
Db 76 KXPDSYDRSTLVAIVVGRLITGMDOALVGMCVNERRLIVPPLHGLSGVAGLAPP 135
QY 129 NSVLHFDVLLMDIWNSEDQVQIHTYFKPPSPRTIQVSDFVRYHYNGTFLDGLTLPDSSHN 188
Db 136 DATLYFDVLLDMVKNKADTVQSTILLRPPYCPRMVQNSDFVRYHYNGTLLDGTAFDNSYS 195
QY 189 RMKTYDVTGVLIPGMDKGLGMCVGEKRIITIPPLAYGEDGDGKDIPOQASLVFV 248
Db 196 RGGYDVTYGSLWIKGMDQGLLGMCPGCKRIIIPPLAYGEKGTGTVIPQASLVFV 255
QY 249 ALLDLHNPKDISIENKVVPCNERISQSGDPLTYHYNGTLLDGLTFDSSYRNRTFDY 308
Db 256 LLLDVHNPKDTVQLETLELPQCQVRAVAGDPMRHYNGSLMDGLTFDSSYRNHTYNTY 315
QY 309 IQGYVITPGMDGLGVCIGKRXIVPPLHGLYGEGRGN-IPGSAVLVFDLHVDFHNP 367
Db 316 VGQGYIIPGMDQGLGACIGERRITVPPHLYAYGNGTGDKIPGSAVLIFDVHVIDFHP 375
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QY 368 SDSISITSHYKPPD-CSVLSSKGDYLYHYNASILDGTLDDSTWNLGKTYNIVLSSGVV 426
Db 376 SDPVEIKTLSPRPNENCNFKTGDFIRHYNCSLDGTGLFSSHDYEAPOEITLGANKVI 435
QY 427 LGMDGLGEMCVGKERTVIIIPHLGYGEAGVDGVPGSVAVLFDIEKLELVAGLPGGYMF 486
Db 436 EGLDRGLQGMCGERRQLIVPPLAHGSGARG-VPPSAVLAFEVELVSRDGLPTGYLP 494
QY 487 IWNGEVSNLFEIDKNGEVLLEEFSEYIIHAQVAGSGKGLAPGDAELIVKNMFTNQD 546
Db 495 VVYQDPSTSLFEDMDLNKDGVEPPPEFSSFIKAQVNEKGRMLPGQDPDKTISDMFQND 554
QY 547 RNGDGKVTABEFLK---XDOEAKHD 568
Db 555 RNQDGKITAEELKLSDEQERVHE 579

RESULT 7
Q9H3N3 PRELIMINARY; PRT; 582 AA.
AC Q9H3N3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 65kDa FK506-binding protein.
GN HKBP65.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RA Ota T., Nishikawa T., Kawai Y., Suzuki Y., Ishii S., Saito K.,
RA Yamamoto J., Sugano S., Isogai T.;
RT "HRI human cDNA sequencing project.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]_TaxID=9606;
RP SEQUENCE FROM N.A.
RA Mitsuomori C., Morikawa N., Isogai T., Ota T., Yuri K., Nishikawa T.,
RA Masuho Y., Nagahara K.;
RT "The human 65kDa FK506-binding protein (HKBP65) gene induces the
  morphological differentiation of NT2 neuron precursor cells.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045981; BAB20974.1; -.
DR HSSP; F20081; IYAT.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000886; ER target.
DR InterPro; IPR001179; FKBP_PPase.
DR Pfam; PF00036; ehand; 2.
DR Pfam; PF00254; FKBP; 4.
DR SMART; SM00054; EFh; 2.
DR PROSITE; PS00018; EF HAND; UNKNOWN 1.
DR PROSITE; PS00014; ER TARGET; UNKNOWN 1.
DR PROSITE; PS00454; FKBP_PPASE 2; UNKNOWN 1.
DR PROSITE; PS00059; FKBP_PPASE 3; 4.
SQ SEQUENCE 582 AA; 64305 MW; 04B25129A1D4D92 CRC64;

Query Match 57.1%; Score 1744; DB 4; Length 582;
Best Local Similarity 56.4%; Pred. No. 1.5e-130;
Matches 326; Conservative 99; Mismatches 131; Indels 22; Gaps 7;

QY 10 PP-----PLILLILLWV-----QAPAVAGLSDAELOIERFVDPDPCRTVRSGLD 55
Db 6 PPSHSLRLPLQLLLLVVQAVGRGLGRASPAGPLED--VIERHYHIPRACPREVQMGD 63
QY 56 FVRYHYVGFPPDQCKDSSYDRSTFNVFVGKGLITGMDOALVGMCVNERFVKIPKPL 115
Db 64 FVRYHYNGTFDGKDFDSSYDRNTLVAIVVGRLITGMDOALVGMCVNERRLIVPPLH 123
QY 116 AYGNERNVSGVIPPNSVHFDVLLMDIWNSEDQVQIHTYFKPPSPRTIQVSDFVRYHYNG 175
Db 124 GYGSIGLAGLIPPDATLYFDVLLDMVKNKEDTVQVSTLLRPPHCPRMVQDGFVRYHYNG 183
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QY 176 TFLDGTFLDSSHNRMKTYDTYVIGWLIIPGMDKGLGKLVGCVGEKRIITIPPFLAYGEDGDG 235
D 184 TLLDGTFFDTSYSGKGYDTYVIGWLIIPGMDKGLGKLVGCVGEKRIITIPPFLAYGEKGYG 243
QY 236 KDIPGOASLVFDVALLDLHNPDKDSISLENKVPENCERISOSGDFLTYHYNGTLLDGTFL 295
D 244 TVIPPOASLVFVHLLIDVHNPDKAVQLETLELPCCVRRAGAGDFMYHYNGSLMDGTFL 303
QY 296 DSSYSNRNPTDYTGQYVIPGMDKGLGKLVGCVGEKRIITIPPFLAYGEKGN-IPGSV 354
D 304 DSSYSNRNPTDYTGQYVIPGMDKGLGKLVGCVGEKRIITIPPFLAYGEKGN-IPGSV 363
QY 355 LVFDIHDVHNPDSISITSHYKPPD-CSVLKKGKLVKYNASLLDGTLLDSTWNLG 413
D 364 LIFNVHVIDFHNPAVDVVEIRTLSPBETCNKTLGDFVRYHNGSLDGTFLTSHDY 423
QY 414 KTYNIVLGSQVVLGMDGLREMCVGEKRTVIIPPHLYGEGAGVDGVPGSVAVLFDIEX 473
D 424 APQEATLGANKVIEGLDTGLQCMCVGERRQLIVPPHLAGESGARG-VPGSAVLFFVEL 482
QY 474 LELVAGLPEGYFIWNGEVSFNLFEEDKNGEVLLEEFSEYTHAQVASKGKLAGPFD 533
D 483 VSREDGLPTGYLFVWHKDPANLFEEDKNGEVLLEEFSEYTHAQVASKGKLAGPFD 542
QY 534 ABLVKNMFTNDRNGDKVTAEEFKL---XDOEAKHD 568
D 543 PEKTIGDMFQNDNRQDKITVDELKLSDEDEERVHE 580

RESULT 8
Q96AY3
ID Q96AY3 PRELIMINARY; PRT; 582 AA.
AC Q96AY3
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Hypothetical 64.2 kDa protein (65 kDa FK506-binding protein)
DE (EC 5.2.1.8).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue=Brain;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RA Tissue=Brain;
RA Rulten S., Kinloch R.A., Robinson C., Gettins L., Kay J.E.;
RT "The Human FK506-Binding Protein Repertoire.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016467; AAH16467.1; -.
DR EMBL; AF337909; AAIL5770.1; -.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000886; EF-hand.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00036; ehand; 2.
DR Pfam; PF0254; FKBP; 4.
DR PROSITE; PS00018; EF HAND; UNKNOWN 1.
DR PROSITE; PS00014; ER TARGET; UNKNOWN 1.
DR PROSITE; PS00454; FKBP_PPIASE 2; UNKNOWN 1.
DR PROSITE; PS00059; FKBP_PPIASE 3; 4.
DR Hypothetical protein; Isomerase.
SQ SEQUENCE 582 AA; 64245 MW; 98257459158407C2 CRC64;

Query Match
Best Local Similarity 56.4%; Pred No. 2.2e-130; Length 582;
Matches 326; Conservative 99; Mismatches 131; Indels 22; Gaps 7;
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QY 10 PP-----PLLLLLLWT-----GOAAPVAGLSDAELQIERRFFVDECPRTVRSGD 55
D 6 PPSHLLRLPLQLLLLVVQVGRGLGRASPAGGLEDD--VVIERYHIPRACPREVQMGD 63
QY 56 FVRVHYVGTTPDGOKFSSYSDRSTFNVGVKGLITGMDQALVGMVCNVERFVKIPPKL 115
D 64 FVRVHYNGTFEDGKFKFSSYSDRNTLVAVVGVRLITGMDRGLMCMCNERRLVPPHL 123
QY 116 AYGNERSVGVPPNSVLHFDVLLMDIWNSEDQVQIHTYFKPPSCPTTIQVSDFVRYHYNG 175
D 124 GYSGIGLAGLIPDATTLYFDVLLDWNKEDTVQVSTLLRPHPCPRMVDGDFVRYHYNG 183
QY 176 TFLDGTFLDSSHNRMKTYDTYVIGWLIIPGMDKGLGKLVGCVGEKRIITIPPFLAYGEDGDG 235
D 184 TLLDGTFFDTSYSGKGYDTYVIGWLIIPGMDKGLGKLVGCVGEKRIITIPPFLAYGEKGYG 243
QY 236 KDIPGOASLVFDVALLDLHNPDKDSISLENKVPENCERISOSGDFLTYHYNGTLLDGTFL 295
D 244 TVIPPOASLVFVHLLIDVHNPDKAVQLETLELPCCVRRAGAGDFMYHYNGSLMDGTFL 303
QY 296 DSSYSNRNPTDYTGQYVIPGMDKGLGKLVGCVGEKRIITIPPFLAYGEKGN-IPGSV 354
D 304 DSSYSNRNPTDYTGQYVIPGMDKGLGKLVGCVGEKRIITIPPFLAYGEKGN-IPGSV 363
QY 355 LVFDIHDVHNPDSISITSHYKPPD-CSVLKKGKLVKYNASLLDGTLLDSTWNLG 413
D 364 LIFNVHVIDFHNPAVDVVEIRTLSPBETCNKTLGDFVRYHNGSLDGTFLTSHDY 423
QY 414 KTYNIVLGSQVVLGMDGLREMCVGEKRTVIIPPHLYGEGAGVDGVPGSVAVLFDIEX 473
D 424 APQEATLGANKVIEGLDTGLQCMCVGERRQLIVPPHLAGESGARG-VPGSAVLFFVEL 482
QY 474 LELVAGLPEGYFIWNGEVSFNLFEEDKNGEVLLEEFSEYTHAQVASKGKLAGPFD 533
D 483 VSREDGLPTGYLFVWHKDPANLFEEDKNGEVLLEEFSEYTHAQVASKGKLAGPFD 542
QY 534 ABLVKNMFTNDRNGDKVTAEEFKL---XDOEAKHD 568
D 543 PEKTIGDMFQNDNRQDKITVDELKLSDEDEERVHE 580

RESULT 9
Q9H6N5
ID Q9H6N5 PRELIMINARY; PRT; 481 AA.
AC Q9H6N5
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE CDNA: FLJ22041 fis, clone HEP09061.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK025694; BAB15220.1; -.
DR HSSP; Q00688; 1PKB.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000886; ER-target.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00036; ehand; 2.
DR Pfam; PF0254; FKBP; 4.
DR SMART; SM00054; EFh; 2.
DR PROSITE; PS00018; EF HAND; UNKNOWN 1.
DR PROSITE; PS00014; ER TARGET; UNKNOWN 1.
DR PROSITE; PS00454; FKBP_PPIASE 2; UNKNOWN 1.
DR PROSITE; PS00059; FKBP_PPIASE 3; 4.
SQ SEQUENCE 481 AA; 53219 MW; A4D5181BFC88BDFD CRC64;
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Query Match 49.8%; Score 1522; DB 4; Length 481;
 Best Local Similarity 57.5%; Pred. No. 5.8e-113;
 Matches 276; Conservative 89; Mismatches 109; Indels 6; Gaps 4;

QY 94 MDQALVGMCMVNERFVKIPKLAYGNERSVGVIPPNVSLHFDVLLMDIWNSEDOVQIHTY 153
 DB 1 MDRLGMCMVNERRLIVPHGLYGSIGLAGLIPPDATLYFDVLLDVWKNEDTVQVSTL 60

QY 154 FKPPSPRTIQVSDVFRYHYNGFLDGLTDFSSSHNRKMTYDVTYVIGWLIPGMDKGLLGM 213
 DB 61 LRPHPCRMVQDGFVRVYHYNGTLLDGTSDTYSKGTGYDVTYVGSGLIKGMDQGLGM 120

QY 214 CVGEKRIITPPPLAYGEDGDKIQOASLVDFDVALLDHNPKDSISIEKNKVPENCER 273
 DB 121 CGERRKIIIPPLAYGEKGYGVIPPOASLVFHVLLIDVHNPKNDAVOLETLELPGCCVR 180

QY 274 ISQSGDFLTHYNGTLLDGLTDFSSYSNRRTFTDYIQGGYVIPGMDGLGVCIGEKRXI 333
 DB 181 RAGAGDFMYHYNGSLMDGLTDFSSYSNRHTYNTYIQGGYIIPGMDQGLQACGERRRI 240

QY 334 VPPPHLYGEGRG-N-IPGSALVFDIHVDHNPSSISITSHYKPPD-CSVLSSKGDY 391
 DB 241 TTPPHLAYGNGTCKIPGSALVIFNVHVIDFHPADVWEIRTLSPSETCNETTKLGD 300

QY 392 LKYHNASLLDGLTDLSTWNLGKTYNIVLGSQGVVLGMDGLREMCVGEKRTVLIIPHLG 451
 DB 301 VRYHNCSLDGLTQFTSHDYGAPQEAATLGANKVIEGLDTGLQGMCGERRQLIVPHLA 360

QY 452 YGAGVDGVPGSALVFDITEXLELVAGLPEGYMFIWNGEVSPLNLFREIDKDGNGEVILLE 511
 DB 361 HGBSGARG-VPGSAVLLFEVLVSREDGLPTGYLFVWHKDPANLPFEDMDLNKDGVEPPE 419

QY 512 EFSEYTHAQVASGKGLAPGDAELIVKNMFTNDRNGDGKVTAEFKL---XDQEAHND 568
 DB 420 EFSTFIKAQVSEKGRMLPGQDPEKTIQDMFQNDQNGDKITVDELKLSDEDEERVHE 479

RESULT 10
 Q9H6J3 PRELIMINARY; PRT; 355 AA.

ID Q9H6J3
 AC Q9H6J3;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE CDNA: FLJ22221 fis, clone HRC01651.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
 RA Suzuki Y., Oabayashi M., Nishi T., Shibahara T., Tanaka T.,
 RA Nakamura Y., Isegai T., Sugano S.;
 RT "NEDO human cDNA sequencing project."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK025874; BAB15266.1; -.
 DR HSSP; Q00688; IPBK.

DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR000886; ER target.
 DR InterPro; IPR001179; FKBP_PPase.
 DR Pfam; PF00036; ehand; 2.
 DR Pfam; PF00254; FKBP; 2.
 DR SMART; SM00054; EFh; 2.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN 1.
 DR PROSITE; PS00014; ER_TARGET; UNKNOWN 1.
 DR PROSITE; PS50059; FKBP_PPASE_3; 2.
 DR PROSITE; PS50059; FKBP_PPASE_3; 2.
 SQ SEQUENCE 355 AA; 38950 MW; DBECF4B8618BF54F CRC64;

Query Match 27.7%; Score 845.5; DB 4; Length 355;
 Best Local Similarity 45.5%; Pred. No. 3.3e-59;
 Matches 161; Conservative 58; Mismatches 68; Indels 67; Gaps 4;

QY 281 LTYHNGTLLDGLTDFSSYSNRRTFTDYIQGGYVIPGMDGLGVCIGEKRXIVVPHLG 340
 DB 1 MRHYNGSLMDGLTDFSSYSNRHTYNTYIQGGYIIPGMDQGLQACGERRITIPPHLA 60

QY 341 YGEGRG-N-IPGSALVFDIHVDHNPSSISITSHYKPPD-CSVLSSKGDY 348
 DB 61 YGEGTDSIGFLQGSAPLRPFSGBGQPSLGRGGYKTEPAYPQDPAVLGASVSSPVKW 120

QY 349 -----IPGSALVFDIHVDHNPSSISITSHYKPPD-CSVLSSKGDY 397
 DB 121 ASHADPQDKIPGSALVIFNVHVIDFHPADVWEIRTLSPSETCNETTKLGDVFRYHYN 180

QY 398 ASLLDGLTDLSTWNLGKTYNIVLGSQGVVLGMDGLREMCVGEKRTVLIIPHLG 457
 DB 181 CSLDGLTQFTSHDYGAPQEAATLGANKVIEGLDTGLQGMCGERRQLIVPHLAGESGA 240

QY 458 DGEVPGSAVLVFDITEXLELVAGLPEGYMFIWNGEVSPLNLFREIDKDGNGEVILLEPSEYI 517
 DB 241 RG-VPGSAVLLFEVLVSREDGLPTGYLFVWHKDPANLPFEDMDLNKDGVEPPEFTFI 299

QY 518 HAQVASGKGLAPGDAELIVKNMFTNDRNGDGKVTAEFKL---XDQEAHND 568
 DB 300 KAQVSEKGRMLPGQDPEKTIQDMFQNDQNGDKITVDELKLSDEDEERVHE 353

RESULT 11
 Q9UF89 PRELIMINARY; PRT; 262 AA.

ID Q9UF89
 AC Q9UF89;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical 28.9 kDa protein (Fragment).

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL131116; CAB61418.1; -.
 DR HSSP; Q00688; IPBK.

DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR000886; ER target.
 DR InterPro; IPR001179; FKBP_PPase.
 DR Pfam; PF00036; ehand; 2.
 DR Pfam; PF00254; FKBP; 2.
 DR SMART; SM00054; EFh; 2.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN 1.
 DR PROSITE; PS00014; ER_TARGET; UNKNOWN 1.
 DR PROSITE; PS50059; FKBP_PPASE_3; 2.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 262 AA; 28926 MW; A9630934276BA84E CRC64;

Query Match 24.1%; Score 736; DB 4; Length 262;
 Best Local Similarity 52.5%; Pred. No. 1.1e-50;
 Matches 137; Conservative 53; Mismatches 65; Indels 6; Gaps 4;

QY 313 YVIPGMDGLGVCIGEKRXIVVPHLGVEEGRN-IPGSALVFDIHVDHNPSSDI 371
 DB 1 YVIPGMDQGLQACGERRITIPPHLAYGNGTCKIPGSALVIFNVHVIDFHPADV 60

QY 372 SITSHYKPPD-CSVLSSKGDYKHYNASLLDGLTDLSTWNLGKTYNIVLGSQGVLLMD 430
 DB 61 EIRTLSPSETCNETTKLGDVFRYHYNCSLLDGLTQFTSHDYGAPQEAATLGANKVIEGLD 120

QY 431 MGLREMCVGEKRTVLIIPHLGVEAGVDGVPGSALVIFVDIEKLELVAGLPEGYMFIWNG 490
 DB 431 MGLREMCVGEKRTVLIIPHLGVEAGVDGVPGSALVIFVDIEKLELVAGLPEGYMFIWNG 490

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Db 121 TGLQMCVGRRLVPPHLAGHSGARG-VPGSAVLFEVLVSREDGLPTGYLFWYHK 179
Qy 491 EVSNLFEEDKCGNGVLEEFSSYTHAQSASGKGLAPGDAELIVKMNFTNDRNGD 550
Db 180 DPPANLFDMDLNKDGVEPPPEFTTFAKQVSEGRGLMPGQDPEKTIGDMFQNRQND 239
Qy 551 GKVTAEFFKL---XDQBAKHD 568
Db 240 GKITVDELKLSDEDESRVHE 260

RESULT 12
Q98UD7 PRELIMINARY; PRT; 137 AA.
AC Q98UD7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE FK506-binding protein (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Anano T., Yoshizato K.;
RT "Isolation of genes involved in intestinal remodeling during anuran
RT metamorphosis."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF170336; AAK11511.1; -.
DR HSP; Q00688; 1PBK.
DR InterPro; IPR001179; FKBP_PPase.
DR Pfam; PF00254; FKBP; 1.
DR PROSITE; PS00454; FKBP_PPASE 2; UNKNOWN_1.
DR PROSITE; PS50059; FKBP_PPASE_3; 1.
FT NON TER 1
FT NON TER 137
SQ SEQUENCE 137 AA; 15070 MW; DC3EGACABB24F625 CRC64;

Query Match 15.2%; Score 464.5; DB 13; Length 137;
Best Local Similarity 65.0%; Pred. No. 1.9e-29;
Matches 89; Conservative 15; Mismatches 32; Indels 1; Gaps 1;

Qy 146 DQVQIHTYFKPSPRTIQVSDVRYHYNGTFLDGTLDSSSHRMKTYDTYVGIGWLIPG 205
Db 1 DEVQITTHKASPCNSRVSQSDSDFVRYHYNGTLDGTLDSSYSRSTTYDTYVGSGLIKG 60
Qy 206 MDKGLLGMVGEKRIITIPPLAYGEDGDKIPQASLVFDVALLDHNPKDSISYENK 265
Db 61 MDMLGLMGACGEKRIITIPPLAYGERGYTIIPAQASLVFHVLLIDFHNPKDGTIVQNG 120
Qy 266 VVPENCERI-SQSGDPL 281
Db 121 VVPGVQTAKATGDIYV 137

RESULT 13
O16309 PRELIMINARY; PRT; 261 AA.
AC O16309;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 29.1 kDa protein.
GN C05C8.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
```

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RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Sammons L., Wohldmann P.;
RT "The sequence of C. elegans cosmid C05C8.";
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF016430; AAB65370.1; -.
DR HSP; P27124; 1ROT.
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001179; FKBP_PPase.
DR Pfam; PF00254; FKBP; 2.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
DR PROSITE; PS00454; FKBP_PPASE 2; UNKNOWN_1.
DR PROSITE; PS50059; FKBP_PPASE_3; 2.
KW Hypothetical protein.
SQ SEQUENCE 261 AA; 29080 MW; 545A8B82B1BE26AD CRC64;

Query Match 11.3%; Score 344.5; DB 5; Length 261;
Best Local Similarity 32.2%; Pred. No. 1.9e-19;
Matches 73; Conservative 51; Mismatches 92; Indels 11; Gaps 4;

Qy 260 ISTENKVPENCERISQSGDPLTYHYNGTLDGTLDSSYSRNRTPDTYIGQGVIPGMD 319
Db 30 IEIKKIGDSKCKIKSESGDLQGFYKLSKEGKVGISNFQ-QPYFTYLGKEVHGME 88
Qy 320 EGLGVCGICGRXIVVPPHLYGEGEGRNIPGSA-VLVFDIHVIDFNP-----SDS 370
Db 89 IAMEGMCVGEQRKVIIPPEQGFQEDG-DEVEGKETLYYFVELKSIIPRPKPAKWITDEG 147
Qy 371 ISTSHYKPPDCSVLSSKGYLVKHYNNASLLDGTLLDSTWNLGKTYNVLGSGGVVLGMD 430
Db 148 VHIHTHEVGCTEKAQAGTLHQQYTLNLEDSFIDSSWRNRPPIFKMGSGGVIKGMD 207
Qy 431 MGLREMCVGEKRTVIIPPHLYGEGAGVDGVEPGSAVLVFDIEKLELV 477
Db 208 IAMEGMCVGEQRKVIIPPELAYGNGRPPAIPGNSYLHFDLSLEKLV 254

RESULT 14
P91180 PRELIMINARY; PRT; 264 AA.
ID P91180
AC P91180;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 29.9 kDa protein.
GN C50F2.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
```


Du Z., Le T.T.;
"The sequence of C. elegans cosmid C50F2.,"
Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.,"
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U80445; AAB37799.1; -.
DR HSPF; P20071; 1B4.
DR InterPro; IPR000886; ER target.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00254; FKBP; 2.
DR PROSITE; PS00014; ER TARGET; UNKNOWN 1.
DR PROSITE; PS00454; FKBP_PPIASE_2; UNKNOWN 2.
DR PROSITE; PS00059; FKBP_PPIASE_3; 2.
KW Hypothetical protein.
SQ SEQUENCE 264 AA; 29937 MW; 90B79FD4FF978A2D CRC64;

Query Match 11.2%; Score 343; DB 5; Length 264;
Best Local Similarity 37.5%; Pred. No. 2.5e-19;
Matches 87; Conservative 36; Mismatches 93; Indels 16; Gaps 7;

QY 142 WNSD--QVQIHTYFKPPSCPRITQVSDFVRYHYNGTFLDGTFLDSSHNRMKTYDYVGI 199
DB 24 WKDEDGLEIKIIRPIKAECPIKSDQDGVLDQWYKLSDKDGKEIGSNFNK-KPYTFTLGK 82

QY 200 GWLIPGMDKGLGMCVGEKRIITIPPLAYGEDGDGKD-IPGQASLVFDVALLDLH--- 254
DB 83 GQVIPGMRAMTGMCKGKRVIPGNLFGDGKGRERDNKEDQTLTYTVQLVDFRAVP 142

QY 255 ----NPKDSISIE--NKVVPENCERISQSGDFTLYHYNGTLLDGTFLDSSYSNRNRTFTDY 308
DB 143 GEKWTDEGIVIEQTHKIDEDCKK-SKSGDTIHQQYVVLHLEDGTFFVDSFSRNAPFIK 201

QY 309 IGQGYVPGMDGLGVCIGEKRXIIVPPHLYGEGRG-NIPGSALVFDI 359
DB 202 LNNNEVIKGMDIAMTGMCEGERRQVVPISDFGYGDDGRAPAIPGKARLYFDI 253

RESULT 15
Q95Q60 PRELIMINARY; PRT; 300 AA.
AC Q95Q60;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 34.2 kDa protein.
GN C50F2.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.,"
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Du Z., Le T.T.;
RT "The sequence of C. elegans cosmid C50F2.,"
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.,"

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U80445; AAK68259.1; -.
DR InterPro; IPR000886; ER target.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00254; FKBP; 2.
DR PROSITE; PS00014; ER TARGET; UNKNOWN 1.
DR PROSITE; PS00454; FKBP_PPIASE_2; UNKNOWN 2.
DR PROSITE; PS00059; FKBP_PPIASE_3; 2.
KW Hypothetical protein.
SQ SEQUENCE 300 AA; 34160 MW; A70252F2736CF36C CRC64;

Query Match 11.2%; Score 343; DB 5; Length 300;
Best Local Similarity 37.5%; Pred. No. 3e-19;
Matches 87; Conservative 36; Mismatches 93; Indels 16; Gaps 7;

QY 142 WNSD--QVQIHTYFKPPSCPRITQVSDFVRYHYNGTFLDGTFLDSSHNRMKTYDYVGI 199
DB 60 WKDEDGLEIKIIRPIKAECPIKSDQDGVLDQWYKLSDKDGKEIGSNFNK-KPYTFTLGK 118

QY 200 GWLIPGMDKGLGMCVGEKRIITIPPLAYGEDGDGKD-IPGQASLVFDVALLDLH--- 254
DB 119 GQVIPGMRAMTGMCKGKRVIPGNLFGDGKGRERDNKEDQTLTYTVQLVDFRAVP 178

QY 255 ----NPKDSISIE--NKVVPENCERISQSGDFTLYHYNGTLLDGTFLDSSYSNRNRTFTDY 308
DB 179 GEKWTDEGIVIEQTHKIDEDCKK-SKSGDTIHQQYVVLHLEDGTFFVDSFSRNAPFIK 237

QY 309 IGQGYVPGMDGLGVCIGEKRXIIVPPHLYGEGRG-NIPGSALVFDI 359
DB 238 LNNNEVIKGMDIAMTGMCEGERRQVVPISDFGYGDDGRAPAIPGKARLYFDI 289

Search completed: April 26, 2003, 06:55:46
Job time : 51.5014 secs

GenCore version 5.1.4 p5.4578
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OM protein - protein search, using sw model

Run on: April 26, 2003, 06:48:54 ; Search time 27.2202 Seconds
(without alignments)
1899.367 Million cell updates/sec

Title: US-09-225-502-8

Perfect score: 2106

Sequence: 1 TYGETGWLIPGMDKGLGMC.....VNDFPLKLLYFTNLNIFVLM 388

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2106	100.0	388	20	AAY23887
2	1616	76.7	570	22	AAB88320
3	1606	76.3	541	20	AAY23886
4	1000.5	47.5	434	21	AAB54356
5	1000.5	47.5	582	21	AAB12128
6	1000.5	47.5	582	21	AAY52294
7	1000.5	47.5	582	22	AAG79226
8	997.5	47.4	441	20	AAY23885
9	771.5	36.6	1241	22	ABG05911
10	618	29.3	127	22	AAO5027

11	544.5	25.9	366	21	AA857114	Human prostate can
12	541.5	25.7	316	20	AAY23884	Amino acid sequenc
13	484.5	23.0	166	23	ABP41125	Human ovarian anti
14	287	13.6	216	22	ABB64697	Drosophila melanog
15	275	13.1	138	22	ABB69722	Drosophila melanog
16	265.5	12.6	159	21	AA810995	Arabidopsis thalia
17	265.5	12.6	163	21	AA810994	Arabidopsis thalia
18	259	12.3	146	21	AA810983	Arabidopsis thalia
19	259	12.3	152	21	AA810987	Arabidopsis thalia
20	259	12.3	153	21	AA810986	Arabidopsis thalia
21	253	12.0	146	21	AA810985	Arabidopsis thalia
22	253	12.0	152	21	AA810984	Arabidopsis thalia
23	253	12.0	153	21	AA810983	Arabidopsis thalia
24	250.5	11.9	163	23	ABG60082	Human DTHP polype
25	247.5	11.8	141	17	AA810985	Human FKBP-13 immu
26	241.5	11.5	137	22	AA810986	Bovine mammary tis
27	237.5	11.3	135	22	AA810987	S cerevisiae apopt
28	236	11.2	143	13	AA810988	hrFKBP. Homo sapi
29	234.5	11.1	211	20	AA810989	Human PRO381 prote
30	234.5	11.1	211	20	AA810990	Polypeptide fragme
31	234.5	11.1	211	21	AA810991	Human PRO381 (UNO3
32	234.5	11.1	211	21	AA810992	Human PRO381 prote
33	234.5	11.1	211	21	AA810993	Human PRO381 prote
34	234.5	11.1	211	21	AA810994	Human PRO381 prote
35	234.5	11.1	211	21	AA810995	Human PRO381 prote
36	234.5	11.1	211	21	AA810996	Human PRO381 prote
37	234.5	11.1	211	21	AA810997	Human PRO381 prote
38	231	11.0	241	22	AA810998	Human colon cancer
39	230.5	10.9	239	21	AA810999	Human cancer assoc
40	227.5	10.8	212	20	AA811001	Secreted protein e
41	225	10.7	219	20	AA811002	Secreted protein e
42	225	10.7	219	20	AA811003	Human secreted pro
43	225	10.7	219	20	AA811004	Human PRO1304 prot
44	225	10.7	222	21	AA811005	Amino acid sequenc
45	225	10.7	222	21	AA811006	Human PRO1304 (UNQ

ALIGNMENTS

RESULT 1

AA811006

ID AAY23887 standard; Protein; 388 AA.

AC AAY23887;

DT 21-SEP-1999 (first entry)

DE Amino acid sequence of a FK506 binding protein 65.

Human; FK506 binding protein; FKBP65; immune system disorder;
immune cell; hematopoietic cell disorder; thrombolytic activity;
blood coagulation disorder; blood platelet disorder; wound;
heart attack; stroke; scarring; autoimmune disorder; allergic reaction;
asthma; allergic asthma; respiratory problem; anaphylaxis;
hypersensitivity; blood group incompatibility; organ rejection;
graft versus host disease; inflammatory condition;
ischemia-reperfusion injury; endotoxin lethality; arthritis;
complement-mediated hyperacute rejection; nephritis; lung injury;
inflammatory bowel disease; Crohn's disease; infection.

OS Homo sapiens.

PN WO9935160-A1.

PD 15-JUL-1999.

PF 06-JAN-1999; 99WO-US00120.

PR 09-JAN-1998; 98US-0070875.

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Moore PA, Ruben SM, Wei Y;
XX WPI; 1999-430382/36.
DR N-PSDB; AAX86148.

XX New nucleic acids encoding human FK506 binding proteins

XX Claim 12; Fig 4; 87pp; English.

XX The present sequence represents a human FK506 binding protein 55
CC (FKBP5). It is a splice variant of the sequence given in AAX86147.
CC The polypeptide or polynucleotide may be useful in treating deficiencies
CC or disorders of the immune system, by activating or inhibiting the
CC proliferation, differentiation, or mobilization (chemotaxis) of immune
CC cells. They may be useful in treating or detecting deficiencies or
CC disorders of hematopoietic cells, to increase differentiation and
CC proliferation of hematopoietic cells including the pluripotent stem
CC cells, in an effort to treat those disorders associated with a decrease
CC in certain types of hematopoietic cells. They can be used to modulate
CC hemostatic or thrombolytic activity, e.g. an increase can treat blood
CC coagulation disorders, blood platelet disorders or wounds resulting from
CC trauma, surgery or other causes, or a decrease can treat heart attacks,
CC strokes or scarring. They can also treat autoimmune disorders, allergic
CC reactions and conditions such as asthma (particularly allergic asthma)
CC or other respiratory problems, anaphylaxis, hypersensitivity to an
CC antigenic molecule, or blood group incompatibility, organ rejection or
CC graft versus host disease, inflammatory conditions, both chronic and
CC acute, including inflammation associated with infection,
CC ischemia-reperfusion injury, endotoxin lethality, arthritis,
CC complement-mediated hyperacute rejection, nephritis, cytokine or
CC chemokine induced lung injury, inflammatory bowel disease, or Crohn's
CC disease. They can also be used to treat viral, bacterial, fungal and
CC parasitic infections.

XX Sequence 388 AA;

Query Match 100.0%; Score 2106; DB 20; Length 388;
Best Local Similarity 100.0%; Pred. No. 9.7e-203;
Matches 388; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TYGEIGWLPKMDKGLGKVCGEKRIITIPFPFLAYGEDGDKIPQASLVPDVALDLH 60
Db 1 TYGEIGWLPKMDKGLGKVCGEKRIITIPFPFLAYGEDGDKIPQASLVPDVALDLH 60
QY 61 NPKDSISTENKVPENCERISQSGDFLRYHYNGTLLDGLTFDSSSRNRTFTYIGQGVV 120
Db 61 NPKDSISTENKVPENCERISQSGDFLRYHYNGTLLDGLTFDSSSRNRTFTYIGQGVV 120
QY 121 IPGMDGGLGVCIGEKRRIVVPHLGYGEGRGNTIPGSAVLVFDIHVIDFHNPSDSISIT 180
Db 121 IPGMDGGLGVCIGEKRRIVVPHLGYGEGRGNTIPGSAVLVFDIHVIDFHNPSDSISIT 180
QY 181 SHYKPPDCSVLSKGDYLYKHYNASLLDGLTLDSTWNLKTNYVLGSGQVVLGMDMGLR 240
Db 181 SHYKPPDCSVLSKGDYLYKHYNASLLDGLTLDSTWNLKTNYVLGSGQVVLGMDMGLR 240
QY 241 EMCVGEKRTVIIPPHLGYGAGVDGVEPGSAVLVFDIELLELVAGLPEGYFIWNGEVSF 300
Db 241 EMCVGEKRTVIIPPHLGYGAGVDGVEPGSAVLVFDIELLELVAGLPEGYFIWNGEVSF 300
QY 301 NLFBEINKVTFCCPVSRRWYPERGQLPQDSNDSPADLIPASWNNHMAFFPLPFPN 360
Db 301 NLFBEINKVTFCCPVSRRWYPERGQLPQDSNDSPADLIPASWNNHMAFFPLPFPN 360
QY 361 GGGTYPEVVNDPFLKLLYFTNLNYFLM 388
Db 361 GGGTYPEVVNDPFLKLLYFTNLNYFLM 388

RESULT.2
AAB88320
ID AAB88320 standard; Protein; 570 AA.
XX

AC AAB88320;

XX 23-MAY-2001 (first entry)

XX Human membrane or secretory protein clone PSEC0007.

XX Human; secretory protein; membrane protein; vaccine; gene therapy;
XX rheumatoid arthritis; diabetes.

XX Homo sapiens.

XX BP1067182-A2.

XX 10-JAN-2001.

XX 07-JUL-2000; 2000EP-0114090.

XX 08-JUL-1999; 99JP-0194179.

XX 11-JAN-2000; 2000JP-0118775.

XX 02-MAY-2000; 2000JP-0183766.

XX (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;

XX WPI; 2001-093989/11.

XX N-PSDB; AAF93747.

XX Nucleic acids encoding secretory proteins/membrane proteins, useful in
XX gene therapy or as candidate target molecules in drug development -

XX Claim 1; SEQ ID 8; 609pp + CD ROM; English.

XX This invention relates to nucleic acid sequences AAF93744 - AAF93916
XX which encode human secretory or membrane proteins represented by
XX AAF88317 - AAF88419. Included in the invention are primers
XX AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the
XX cDNA sequences of the invention. The invention also includes methods for
XX the production of antibodies directed against the proteins, and cDNA
XX sequences, which can be used in vaccines. The polynucleotide sequences
XX can be used in gene therapy. The polynucleotide sequences and the
XX proteins they encode may be used in the prevention, treatment and
XX diagnosis of diseases associated with inappropriate secretory
XX protein/membrane protein expression. The nucleic acids and complementary
XX sequences may also be used as DNA probes in diagnostic assays
XX (e.g. polymerase chain reactions (PCR)) to detect and quantitate the
XX presence of similar nucleic acid sequences in samples. They may also be
XX used to study the expression and function of secretory proteins/membrane
XX polypeptides and their role in metabolism. The polypeptides may be used
XX as antigens in the production of antibodies against them and in assays to
XX identify modulators (agonists and antagonists) of expression and
XX activity. The antibodies and antagonists may also be used as therapeutic
XX agents to down regulate expression and activity. The antibodies may also
XX be used as diagnostic agents for detecting the presence of the
XX polypeptides in samples (e.g. by enzyme linked immunosorbent assay
XX (ELISA). Examples of diseases which may be treated include rheumatoid
XX arthritis and diabetes.

XX Sequence 570 AA;

Query Match 76.7%; Score 1616; DB 22; Length 570;
Best Local Similarity 99.7%; Pred. No. 3e-153;
Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TYGEIGWLPKMDKGLGKVCGEKRIITIPFPFLAYGEDGDKIPQASLVPDVALDLH 60
Db 195 TYVGIGWLPKMDKGLGKVCGEKRIITIPFPFLAYGEDGDKIPQASLVPDVALDLH 254
QY 61 NPKDSISTENKVPENCERISQSGDFLRYHYNGTLLDGLTFDSSSRNRTFTYIGQGVV 120
Db 255 NPKDSISTENKVPENCERISQSGDFLRYHYNGTLLDGLTFDSSSRNRTFTYIGQGVV 314
QY 121 IPGMDGGLGVCIGEKRRIVVPHLGYGEGRGNTIPGSAVLVFDIHVIDFHNPSDSISIT 180

Db 315 IFGMDGGLGVCIGEKRRIVVPHLGYGEGRGNI PGSAVLVFDIHFVDFHNPDSISIT 374
 Qy 181 SHYKPPDCSVLSKKGDLKHYHNASLLDGLTLDSTWNLGKTYNIVLGGQVVLGMDMGLR 240
 Db 375 SHYKPPDCSVLSKKGDLKHYHNASLLDGLTLDSTWNLGKTYNIVLGGQVVLGMDMGLR 434
 Qy 241 EMCVGEKRTVIIIPHLGYGAGVDEVP GS AVL VFDIELLELVAGLPEGYMFVWNGEVSP 300
 Db 435 EMCVGEKRTVIIIPHLGYGAGVDEVP GS AVL VFDIELLELVAGLPEGYMFVWNGEVSP 494
 Qy 301 NLFEEINK 308
 Db 495 NLFEEIDK 502
 RESULT 3
 AAY23886
 ID AAY23886 standard; Protein; 541 AA.
 AC AAY23886;
 XX
 DT 21-SEP-1999 (first entry)
 XX
 DE Amino acid sequence of a FK506 binding protein.
 XX
 KW Human; FK506 binding protein; FKBP65; immune system disorder;
 KW immune cell; hematopoietic cell disorder; thrombolytic activity;
 KW blood coagulation disorder; blood platelet disorder; wound;
 KW heart attack; stroke; scarring; autoimmune disorder; allergic reaction;
 KW asthma; allergic asthma; respiratory problem; anaphylaxis;
 KW hypersensitivity; blood group incompatibility; organ rejection;
 KW graft versus host disease; inflammatory condition;
 KW ischemia-reperfusion injury; endotoxin lethality; arthritis;
 KW complement-mediated hyperacute rejection; nephritis; lung injury;
 KW inflammatory bowel disease; Crohn's disease; infection.
 XX
 OS Homo sapiens.
 XX
 PN WO9935160-A1.
 XX
 PD 15-JUL-1999.
 XX
 PF 06-JAN-1999; 99WO-US00120.
 XX
 PR 09-JAN-1998; 98US-0070875.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Moore PA, Ruben SM, Wei Y;
 XX
 DR WPI; 1999-430382/36.
 DR N-PSDB; AAX86147.
 XX
 PT New nucleic acids encoding human FK506 binding proteins
 XX
 PS Claim 12; Fig 3; 87pp; English.
 XX
 CC The present sequence represents human FK506 binding protein 65 (FKBP65).
 CC The polypeptide or polynucleotide may be useful in treating deficiencies
 CC or disorders of the immune system, by activating or inhibiting the
 CC proliferation, differentiation, or mobilization (chemotaxis) of immune
 CC cells. They may be useful in treating or detecting deficiencies or
 CC disorders of hematopoietic cells, to increase differentiation and
 CC proliferation of hematopoietic cells including the pluripotent stem
 CC cells, in an effort to treat those disorders associated with a decrease
 CC in certain types of hematopoietic cells. They can be used to modulate
 CC hemostatic or thrombolytic activity, e.g. an increase can treat blood
 CC coagulation disorders, blood platelet disorders or wounds resulting from
 CC trauma, surgery or other causes, or a decrease can treat heart attacks,
 CC strokes or scarring. They can also treat autoimmune disorders, allergic
 CC reactions and conditions such as asthma (particularly allergic asthma) or
 CC other respiratory problems, anaphylaxis, hypersensitivity to an antigenic

CC molecule, or blood group incompatibility, organ rejection or graft versus
 CC host disease, inflammatory conditions, both chronic and acute, including
 CC inflammation associated with infection, ischemia-reperfusion injury,
 CC endotoxin lethality, arthritis, complement-mediated hyperacute rejection,
 CC nephritis, cytokine or chemokine induced lung injury, inflammatory bowel
 CC disease, or Crohn's disease. They can also be used to treat viral,
 CC bacterial, fungal and parasitic infections.
 XX

SQ Sequence 541 AA;

Query Match 76.3%; Score 1606; DB 20; Length 541;
 Best Local Similarity 98.1%; Pred. No. 2.8e-152;
 Matches 302; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TYGEIGWLIPGMDKGLLGMVCVGEKRIITIPFLAYGEDGDKIPQASLVFVALLDLH 60
 Db 195 TVVGIGWLIPGMDKGLLGMVCVGEKRIITIPFLAYGEDGDKIPQASLVFVALLDLH 254
 Qy 61 NPKDSISITENKVPENCERISQSGDFLRVHYNGTLLDGLTLDSTWNLGKTYNIVLGGQV 120
 Db 255 NPKDSISITENKVPENCERISQSGDFLTHYNGTLLDGLTLDSTWNLGKTYNIVLGGQV 314
 Qy 121 IFGMDGGLGVCIGEKRRIVVPHLGYGEGRGNI PGSAVLVFDIHFVDFHNPDSISIT 180
 Db 315 IFGMDGGLGVCIGEKRRIVVPHLGYGEGRGNI PGSAVLVFDIHFVDFHNPDSISIT 374
 Qy 181 SHYKPPDCSVLSKKGDLKHYHNASLLDGLTLDSTWNLGKTYNIVLGGQVVLGMDMGLR 240
 Db 375 SHYKPPDCSVLSKKGDLKHYHNASLLDGLTLDSTWNLGKTYNIVLGGQVVLGMDMGLR 434
 Qy 241 EMCVGEKRTVIIIPHLGYGAGVDEVP GS AVL VFDIELLELVAGLPEGYMFVWNGEVSP 300
 Db 435 EMCVGEKRTVIIIPHLGYGAGVDEVP GS AVL VFDIELLELVAGLPEGYMFVWNGEVSP 494
 Qy 301 NLFEEINK 308
 Db 495 NLFEEIDK 502

RESULT 4

AAB54356
 ID AAB54356 standard; Protein; 434 AA.

AC AAB54356;

XX 09-MAR-2001 (first entry)

XX Human pancreatic cancer antigen protein sequence SEQ ID NO:808.

DE Human; pancreas; pancreatic cancer; pancreatic cancer antigen;
 KW detection; diagnosis; identification; cytostatic; neuroprotective;
 KW neotropic; immunomodulatory; relaxant; contraceptive; gynaecological;
 KW antinflammatory; cardiac; gene therapy; chromosome mapping;
 KW linkage analysis; tissue identification; tissue typing; forensic;
 KW neural; immune system; muscular; reproductive; gastrointestinal;
 KW pulmonary; cardiovascular; renal; proliferative.

XX Homo sapiens.

XX WO200055320-A1.

XX 21-SEP-2000.

XX 08-MAR-2000; 2000WO-US05989.

XX 12-MAR-1999; 99US-0124270.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPI; 2000-579444/54.

DR N-PSDB; AAC99121.

XX New nucleic acid that is a pancreatic cancer antigen for preventing,
 PT treating, or ameliorating a medical condition, particular pancreatic
 PT cancer, or for use in assays for diagnosing a pathological condition -
 XX
 XX
 XX Claim 11; Page 1260-1261; 1379pp; English.
 XX
 CC AAC98773 to AAC99231 encode the human pancreatic cancer associated
 CC proteins, called pancreatic cancer antigens, given in AAB54008 to
 CC AAB54466. The human pancreatic cancer antigens have cytostatic,
 CC gynaecological, nontropic, immunomodulatory, relaxant, contraceptive,
 CC neuroprotective, cardiac and antiinflammatory activities, and can be used
 CC in gene therapy. The polynucleotide and proteins can be used for
 CC preventing, treating, or ameliorating a medical condition or in assays
 CC for diagnosing a pathological condition or a susceptibility to one in a
 CC subject. Binding partners to the proteins and the activity of the
 CC proteins can be identified. The pancreatic cancer antigens can be used to
 CC detect, treat or prevent pancreatic disorders, especially cancer.
 CC Agonists and antagonists to the antigens can be screened for. The
 CC pancreatic cancer antigen polynucleotides can be used to design nucleic
 CC acid hybridisation probes that can be used in chromosome mapping, linkage
 CC analysis, tissue identification and/or typing and a variety of forensic
 CC and diagnostic methods. The proteins can be used to generate antibodies
 CC which are used to purify, detect and target the polypeptides, including
 CC both in vivo and in vitro diagnostic and therapeutic methods. The
 CC proteins can be used to treat or prevent neural, immune system, muscular,
 CC reproductive, gastrointestinal, pulmonary, cardiovascular, renal or
 CC proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
 CC sequences used in the exemplification of the present invention.
 XX
 XX Sequence 434 AA;

Query Match 47.5%; Score 1000.5; DB 21; Length 434;
 Best Local Similarity 55.1%; Pred. No. 1.4e-91;
 Matches 189; Conservative 60; Mismatches 73; Indels 21; Gaps 6;

Qy 1 TYGEIGWLPMDKGLGMCVGEKRIITPPFLAYGEDGDKDIPQASLVDFVALLDLH 60
 Db 55 TVGSGWLIKMDQGLGMCVGERKIIIPFLAYGEKGYVIPPQASLVDFVALLDLH 114
 Qy 61 NPKDSISENKVVPENCERISQSGDFLRHYNGTLLDGTLPDSSYSRNRFTDYIGQYV 120
 Db 115 NPKDAVQLETLPPGCVRRAGAGDFMRHYNGSLMDGTLPDSSYSRNRFTDYIGQYV 174
 Qy 121 IPGMDGGLGVCIGEKRRIVPPHLYGEGRGN-IPGSALVDFIDHFNPSDSISI 179
 Db 175 IPGMDQGLQACMGERRITIPFLAYGNGTGDKIPGSALVDFIDHFNPSDSISI 234
 Qy 180 TSHYKPPD-CSVLSKKGDKLVKHYNASLLDGTLLDSTWNLGKTYNIVLGSQGVLMGDMG 238
 Db 235 RTLSRPSETCNETTKLGDVFRHYNCSLLDGTQLFTSHDYGAPQEAATLGANKVIEGLDTG 294
 Qy 239 IREMCVGEKRTVIIPPHLYGEGAGVDGVPGSALVDFIDHFNPSDSISI 298
 Db 295 LQGMCGVRRQLIVPPHLYGEGAGV-VPGSALVDFIDHFNPSDSISI 353
 Qy 299 SPNLFEE--EINK-----VTFCCPFVSWRRWYPEGKGL 330
 Db 354 PANLFEDMDLNKDGVEPPPEFTFI-----KAQVSEKGL 389

RESULT 5

AAB12128
 ID AAB12128 standard; Protein; 582 AA.
 XX
 AC AAB12128;
 XX
 DT 02-FEB-2001 (first entry)
 XX
 DE Hydrophobic domain protein from clone HP02991 isolated from KB cells.
 XX
 KW Human; secreted protein; membrane protein; hydrophobic domain;
 KW proliferation control; differentiation induction; material transport;

KW biophylaxis; signal receptor; ion channel; transporter; immunostimulant;
 KW immunosuppressant; haematopoiesis regulator; chemotactic; chemokinetic;
 KW haemostatic; thrombolytic; anti-inflammatory; tumour inhibition;
 KW autoimmune disease; Alzheimer's disease; Parkinson's disease; cancer.
 XX
 OS Homo sapiens.
 XX
 PN W0200029448-A2.
 XX
 PD 25-MAY-2000.
 XX
 PF 17-NOV-1999; 99WO-JP06412.
 XX
 PR 17-NOV-1998; 98JP-0326255.
 PR 22-DEC-1998; 98JP-0364315.
 PR 16-MAR-1999; 99JP-0069811.
 PR 27-APR-1999; 99JP-0119299.
 PR 19-MAY-1999; 99JP-0138169.
 XX
 PA (SAGA) SAGAMI CHEM RES CENT.
 PA (PROT-) PROTEGENE INC.
 XX
 PI Kato S, Kimura T;
 XX
 DR WPI; 2000-387753/33.
 DR N-PSDB; AAA62001, AAA62011.
 XX
 PT Proteins comprising hydrophobic regions, such as secretory and membrane
 PT proteins, useful in research and diagnostics and having various
 PT activities e.g. immunomodulatory, antiinflammatory, chemokinetic,
 PT haemostatic, thrombolytic -
 XX
 PS Claim 1; Page 230-232; 410pp; English.
 CC
 CC Secretory proteins play important roles in the proliferation control, the
 CC differentiation induction, the material transport and the biophylaxis of
 CC cells. Membrane proteins have important roles as signal receptors, ion
 CC channels and transporters. The present sequence is a human protein which
 CC has at least one hydrophobic domain. This protein may be a secretory or a
 CC membrane protein. The present protein may have cytokine and cell
 CC proliferation/differentiation activity, immune stimulating or suppressing
 CC activity, haematopoiesis activity, tissue growth activity,
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, anti-inflammatory activity and tumour
 CC inhibition activity. The present protein could therefore be used for
 CC treatment of autoimmune disease, Alzheimer's disease, Parkinson's
 CC disease, and cancer.
 XX
 SQ Sequence 582 AA;

Query Match 47.5%; Score 1000.5; DB 21; Length 582;
 Best Local Similarity 55.1%; Pred. No. 2.2e-91;
 Matches 189; Conservative 60; Mismatches 73; Indels 21; Gaps 6;

Qy 1 TYGEIGWLPMDKGLGMCVGEKRIITPPFLAYGEDGDKDIPQASLVDFVALLDLH 60
 Db 203 TVGSGWLIKMDQGLGMCVGERKIIIPFLAYGEKGYVIPPQASLVDFVALLDLH 262
 Qy 61 NPKDSISENKVVPENCERISQSGDFLRHYNGTLLDGTLPDSSYSRNRFTDYIGQYV 120
 Db 263 NPKDAVQLETLPPGCVRRAGAGDFMRHYNCSLLDGTQLFTSHDYGAPQEAATLGANKVIEGLDTG 322
 Qy 121 IPGMDGGLGVCIGEKRRIVPPHLYGEGRGN-IPGSALVDFIDHFNPSDSISI 179
 Db 323 IPGMDQGLQACMGERRITIPFLAYGNGTGDKIPGSALVDFIDHFNPSDSISI 382
 Qy 180 TSHYKPPD-CSVLSKKGDKLVKHYNASLLDGTLLDSTWNLGKTYNIVLGSQGVLMGDMG 238
 Db 383 RTLSRPSETCNETTKLGDVFRHYNCSLLDGTQLFTSHDYGAPQEAATLGANKVIEGLDTG 442
 Qy 239 IREMCVGEKRTVIIPPHLYGEGAGVDGVPGSALVDFIDHFNPSDSISI 298
 Db 443 LQGMCGVRRQLIVPPHLYGEGAGV-VPGSALVDFIDHFNPSDSISI 501

QY	1	TYGEIGWLIPGMQKLLGCMVGSKRIITTPPFLAYGSDGDKHDPQASLIVFDVALLDLH	60
DB	203	TYVCSGLIKGMDQGLLGCMGPERKIIIPFLAYGKGYGTVPQASLVFHVLLDVH	262
QY	61	NPKDSISIKNKPENCERISQSGDFLRYHYNGTLLDGLTFDSYSNRNFTDTYIGGVY	120

CC hemostatic or

The present sequence represents a human FK506 binding protein 65 (FKBP65). It is a splice variant of the sequence given in AA86145. The polypeptide or polynucleotide may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilization (chemotaxis) of immune cells. They may be useful in treating or detecting deficiencies or disorders of hematopoietic cells, to increase differentiation and proliferation of hematopoietic cells including the pluripotent stem cells, in an effort to treat those disorders associated with a decrease in certain types of hematopoietic cells. They can be used to modulate hemostatic or thrombolytic activity, e.g. an increase can treat blood coagulation disorders, blood platelet disorders or wounds resulting from

OS Homo sapiens.
 PN WO200164835-A2.
 XX
 PD 07-SEP-2001.
 XX
 PF 26-FEB-2001; 2001WO-US04927.
 XX
 PF 28-FEB-2000; 2000US-0515126.
 XX
 PR 18-MAY-2000; 2000US-0577409.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 XX Tang YT, Liu C, Drmanac RT;
 PI WPI; 2001-514838/56.
 XX N-PSDB; AAI84958.
 DR
 DR Isolated nucleic acids and polypeptides, useful for preventing
 XX diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -
 XX
 XX Claim 20; SEQ ID NO 18919; 1399pp + Sequence Listing; English.
 PS
 XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX SQ Sequence 127 AA;
 Query Match 29.3%; Score 618; DB 22; Length 127;
 Best Local Similarity 97.5%; Pred. No. 6e-54;
 Matches 117; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 189 SVLSKGGDYLYKHYNASLLDGLTLLDSTWNLGKTYNVLGSGQVVLGMDGLREMCVGER 248
 DB 2 SVLSKGGDYLYKHYNASLLDGLTLLDSTWNLGKTYNVLGSGQVVLGMDGLREMCVGER 61
 QY 249 TVIIPPHLYGAGVDGEVPGSAVLVDFDLELLELVAGLPEGYNFIWNGEVSFNLFEINK 308
 DB 62 TVIIPPHLYGAGVDGEVPGSAVLVDFDLELLELVAGLPEGYNFIWNGEVSFNLFEIDK 121
 RESULT 11
 AAB57114
 ID AAB57114 standard; Protein; 366 AA.
 XX
 AC AAB57114;
 XX
 DT 13-MAR-2001 (first entry)
 XX
 DE Human prostate cancer antigen protein sequence SEQ ID NO:1692.
 XX
 KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
 KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
 KW vulnery; gastrointestinal; nephrotropic; antiinfective; gynaecological;
 KW antibacterial; gene therapy; neural; immune; reproductive; renal;
 KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
 KW wound; infectious disease.
 XX
 OS Homo sapiens.
 XX

PN WO200055174-A1.
 XX
 PD 21-SEP-2000.
 XX
 PF 08-MAR-2000; 2000WO-US05988.
 XX
 PR 12-MAR-1999; 99US-0124270.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA (ROSE/) ROSEN C A.
 XX
 XX Rosen CA, Ruben SM;
 PI WPI; 2000-587513/55.
 XX N-PSDB; AAI16317.
 XX
 XX Prostate cancer associated gene sequences, referred to as prostate
 PT cancer antigens, useful for treatment, prevention, and diagnosis of
 XX disorders such as prostate cancer -
 XX
 XX Claim 11; Page 2162-2164; 2338pp; English.
 PS
 XX AAI15566 to AAI16505 encode the human prostate cancer associated
 CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
 CC The prostate cancer antigens can have neuroprotective, cytostatic,
 CC cardioactive, immunomodulatory, muscular, vulnery, gastrointestinal,
 CC nephrotropic, antiinfective, gynaecological and antibacterial activities,
 CC and can be used in gene therapy. The prostate cancer antigen
 CC polynucleotides may be used for detection of prostate cancer, chromosome
 CC identification, as chromosome markers, and for numerous other diagnostic
 CC or research purposes. The prostate cancer antigens may be used to treat
 CC disorders such as neural, immune, muscular, reproductive,
 CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
 CC disorders, wounds, and infectious diseases. AAI16506 to AAI16514 to
 CC AAB57303 represent sequences used in the exemplification of the present
 CC invention.
 XX
 XX SQ Sequence 366 AA;
 Query Match 25.9%; Score 544.5; DB 21; Length 366;
 Best Local Similarity 48.5%; Pred. No. 7.2e-46;
 Matches 98; Conservative 37; Mismatches 66; Indels 1; Gaps 1;
 QY 62 PKDSISINIKVVPNCERISQSGDFLRHYNGTLLDGLTDFSSYSRNRFTPTIYIQGGYVI 121
 DB 76 FLEDVIERVHI PRACPREVQMGDFVRYHYNGTFEDGKGFSSYDRNTLVAIVGVGRLLI 135
 QY 122 PQMDEGLLCVIGEKRRIVVPVPHLYGEGE-RGNIPGSAVLVDFDHFNPDSISIT 180
 DB 136 TQMDRGLMGMCNRRRLIVPPHLYGYSIGLAGLIPPDATLYFDVLLDVWVKEDTVQVS 195
 QY 181 SHYKPPDCSVLSKGGDYLYKHYNASLLDGLTLLDSTWNLGKTYNVLGSGQVVLGMDGLR 240
 DB 196 TLLRPPHPCRMVQMGDFVRYHYNGTLLDSTFDSYSKGGTYDYVGSGLIKGNDQGLL 255
 QY 241 EMCVGERKTVIIPPHLYGEGAG 262
 DB 256 GMPGERKRIIPPPFLAYGERG 277
 RESULT 12
 AAY23884
 ID AAY23884 standard; Protein; 316 AA.
 XX
 AC AAY23884;
 XX
 DT 21-SEP-1999 (first entry)
 XX
 DE Amino acid sequence of FK506 binding protein 65 (FKBP65).
 XX
 KW Human; FK506 binding protein; FKBP65; immune system disorder;
 KW immune cell; hematopoietic cell disorder; thrombolytic activity;
 KW blood coagulation disorder; blood platelet disorder; wound;

KW heart attack; stroke; scarring; autoimmune disorder; allergic reaction;
 KW asthma; allergic asthma; respiratory problem; anaphylaxis;
 KW hypersensitivity; blood group incompatibility; organ rejection;
 KW graft versus host disease; inflammatory condition;
 KW ischemia-reperfusion injury; endotoxin lethality; arthritis;
 KW complement-mediated hyperacute rejection; nephritis; lung injury;
 KW inflammatory bowel disease; Crohn's disease; infection.

XX Homo sapiens.

XX WO9935160-A1.

XX 15-JUL-1999.

XX 06-JAN-1999; 99WO-US00120.

XX 09-JAN-1998; 98US-0070875.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Moore PA, Ruben SM, Wei Y;

XX WPI; 1999-430382/36.

XX N-PSDB; AAX86145.

XX New nucleic acids encoding human FK506 binding proteins

XX Claim 12; Fig 1; 87pp; English.

XX The present sequence represents human FK506 binding protein 65 (FKBP65).
 CC The polypeptide or polynucleotide may be useful in treating deficiencies
 CC or disorders of the immune system, by activating or inhibiting the
 CC proliferation, differentiation, or mobilization (chemotaxis) of immune
 CC cells. They may be useful in treating or detecting deficiencies or
 CC disorders of hematopoietic cells, to increase differentiation and
 CC proliferation of hematopoietic cells including the pluripotent stem
 CC cells, in an effort to treat those disorders associated with a decrease
 CC in certain types of hematopoietic cells. They can be used to modulate
 CC hemostatic or thrombolytic activity, e.g. an increase can treat blood
 CC coagulation disorders, blood platelet disorders or wounds resulting from
 CC trauma, surgery or other causes, or a decrease can treat heart attacks,
 CC strokes or scarring. They can also treat autoimmune disorders, allergic
 CC reactions and conditions such as asthma (particularly allergic asthma) or
 CC other respiratory problems, anaphylaxis, hypersensitivity to an antigenic
 CC molecule, or blood group incompatibility, organ rejection or graft versus
 CC host disease, inflammatory conditions, both chronic and acute, including
 CC inflammation associated with infection, ischemia-reperfusion injury,
 CC endotoxin lethality, arthritis, complement-mediated hyperacute rejection,
 CC nephritis, cytokine or chemokine induced lung injury, inflammatory bowel
 CC disease, or Crohn's disease. They can also be used to treat viral,
 CC bacterial, fungal and parasitic infections.

XX Sequence 316 AA;

Query Match 25.7%; Score 541.5; DB 20; Length 316;
 Best Local Similarity 48.0%; Pred. No. 1.2e-45;
 Matches 97; Conservative 38; Mismatches 66; Indels 1; Gaps 1;

QY 62 PKOSISIKVVPNCERISQSGPLRVHYNGTLLDGTLPSSYSRNRFTDYIGQYVI 121

Db 40 PLEDWIERVHIPRACPREVQMGDFRVHYNGTFEDGKKFSSYDRNTLVAIVVGGRLL 99

QY 122 PGMDEGLLVCTGKRRVTPPHLGYGEG-RGNTPGSNVLVFDTHVDHFNPSISIT 180

Db 100 TGMDRGLMGCMVNRRLVPPHLGYGIGLAGLPPDNTLFDVLLDWNKEDTVQVS 159

QY 181 SHYKPPDCSVLSKKGDKLYKHYNASLLDGTLLDSTNWKGTNYIVLGSQVVLGMDGLR 240

Db 160 TLLRPPHCPRVQDGFVRHYNGTLLDGTSPDTSYSGKGYDTYVGSGLIKMGMDQGLL 219

QY 241 EMCVGKRTVLIIPPHLGYGEG 262

Db 220 GMPGQRKIIIPPLAYGEG 241

RESULT 13

ABP411125

ID ABP411125 standard; Protein; 166 AA.

XX ABP411125;

XX 23-AUG-2002 (first entry)

XX Human ovarian antigen HOFMO23, SEQ ID NO:2257.

XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 XX ovarian cancer; breast cancer; reproductive system disorder;
 XX infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 XX PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
 XX inflammatory condition; immune disorder; blood disorder;
 XX gastrointestinal disorder; respiratory disorder; neurological disorder;
 XX cardiovascular disorder; urinary system disorder; drug screening;
 XX gene therapy; chromosome mapping; forensic analysis;
 XX antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 XX antiinflammatory; gynaecological; reproductive.

XX Homo sapiens.

XX WO200200677-A1.

XX 03-JAN-2002.

XX 07-JUN-2001; 2001WO-US18569.

XX 07-JUN-2000; 2000US-209467P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Birse CE, Rosen CA;

XX WPI; 2002-147878/19.

XX N-PSDB; ABQ54202.

XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 XX useful in the prevention, treatment and diagnosis of cancer (e.g.
 XX ovarian cancer), immune disorders, cardiovascular disorders and
 XX neurological diseases -

XX Claim 11; SEQ ID No 2257; 2922pp; English.

XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
 XX ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 XX encompasses polypeptides 90% identical and polynucleotides 95% identical
 XX to the sequences of the invention. The invention additionally relates to
 XX recombinant vectors and host cells comprising human ovarian antigen
 XX polynucleotides, antibodies against human ovarian antigens, and the use
 XX of ovarian antigen polynucleotides and polypeptides in diagnosing,
 XX treating, prognosing or preventing various ovary and/or breast-related
 XX disorders. Such conditions include ovarian cancer and breast cancer, and
 XX metastatic tumours of ovarian or breast origin, reproductive system
 XX disorders (e.g., infertility, disorders of pregnancy, anovulation,
 XX polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine
 XX disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 XX shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 XX vaginitis), immune disorders (e.g., congenital and acquired
 XX immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 XX blood-related disorders (e.g., anaemia), cardiovascular disorders,
 XX respiratory disorders, neurological disorders, gastrointestinal disorders
 XX and urinary system disorders. Ovarian antigen polypeptides and
 XX polynucleotides may also be used in screening for compounds which
 XX modulate ovarian antigen expression or activity. The polynucleotides may
 XX further be used for gene therapy, chromosome mapping, in the
 XX identification of individuals and in forensic analysis, and the
 XX polypeptides may be used as food additives or to prepare antibodies
 XX useful in disease diagnosis, drug targeting and phenotyping. The present
 XX sequence represents a human ovarian antigen of the invention.

CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 166 AA;

Query Match 23.0%; Score 484.5; DB 23; Length 166;
 Best Local Similarity 54.9%; Pred. No. 2.3e-40;
 Matches 89; Conservative 27; Mismatches 45; Indels 1; Gaps 1;
 QY 25 RIITIPPLAYGEGDGKDIQASLVDFVALLDHNPKDSISIEKNVVPENCERISQSG 84
 DB 4 RUVKIPPLAYGEGVGVPDPSVLFHFDVLLWNSDQVQVHTYFTPPSCRTIQVX 63
 QY 85 DELRYHNGTLTDLGTFDSSYSNRRTDTYIGGVIPQMDGGLGVCIGEKRRIVVPPH 144
 DB 64 DFVRHYNGTFLDGLTFDSSHNRMKTYDTVGWLGWLPMDKGLGVCIGEKRIITIPP 123
 QY 145 LQYGEGRG-NIPGSALVDFDIHVDHNPDSISITSHYKP 185
 DB 124 LAYGEGDGKDIQASLVDFVALLDHNPKDSISIEKNVVP 165

RESULT 14

ABB64697
 ID ABB64697 standard; Protein; 216 AA.

XX AC ABB64697;
 XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster polypeptide SEQ ID NO 20883.
 XX KW Drosophila; developmental biology; cell signalling; insecticide;
 XX OS Drosophila melanogaster.
 XX PN WO200171042-A2.
 XX PD 27-SEP-2001.

XX PF 23-MAR-2001; 2001WO-US09231.
 XX PR 23-MAR-2000; 2000US-191637P.
 XX PR 11-JUL-2000; 2000US-0614150.
 XX PA (PEKE) PE CORP NY.
 XX PI Venter JC, Adams M, Li PWD, Myers EW;
 XX DR WPI; 2001-656860/75.
 XX DR N-PSDB; ABL08800.

XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
 XX genes from Drosophila and for elucidating cell signalling and cell-cell
 XX interactions -
 XX PS Disclosure; SEQ ID NO 20883; 21pp + Sequence Listing; English.
 XX CC The invention relates to an isolated nucleic acid detection reagent
 XX capable of detecting 1000 or more genes from Drosophila. The invention is
 XX useful in developmental biology and in elucidating cell signalling and
 XX cell-cell interactions in higher eukaryotes for the development of
 XX insecticides, therapeutics and pharmaceutical drugs. The invention
 XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 XX sequences (ABL01840-ABL16175) and the encoded proteins
 XX (ABBS7737-ABBS72072).

XX CC The sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic format directly from WIPO
 XX at ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 216 AA;

Query Match 13.6%; Score 287; DB 22; Length 216;
 Best Local Similarity 37.4%; Pred. No. 2.4e-20;
 Matches 65; Conservative 31; Mismatches 54; Indels 24; Gaps 5;

QY 47 QASLVDFVALLDHNPKDSISIEKNV-----PENCERISQSGDPLRYHNGT 94
 DB 3 KSNLVISCLLL-----VAISNLVRAQDLKVEIVISTEVCQKSKNGDSLTMHTGT 54
 QY 95 L-LDGTLPDSSYSNRRTDTYIGGVIPQMDGGLGVCIGEKRRIVVPPHLYGEGRG 153
 DB 55 LQDKKKPDSFDRDQPTFQAGQVIGWQGLANCMVGEKRRITIPQGLGVDQAG 114
 QY 154 N-IPGSALVDFDIHVDHNPDSISITSHYKPPDCSVLSK--GDYLYHYNA 204
 DB 115 NVIPPKATLFDVELINIGNAPPTTNVFKIEDDNADKQLSRESEVYLKKQMTA 168

RESULT 15

ABB69722
 ID ABB69722 standard; Protein; 138 AA.

XX AC ABB69722;
 XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster polypeptide SEQ ID NO 35958.
 XX KW Drosophila; developmental biology; cell signalling; insecticide;
 XX OS Drosophila melanogaster.
 XX PN WO200171042-A2.
 XX PD 27-SEP-2001.

XX PF 23-MAR-2001; 2001WO-US09231.
 XX PR 23-MAR-2000; 2000US-191637P.
 XX PR 11-JUL-2000; 2000US-0614150.
 XX PA (PEKE) PE CORP NY.
 XX PI Venter JC, Adams M, Li PWD, Myers EW;
 XX DR WPI; 2001-656860/75.
 XX DR N-PSDB; ABL13825.

XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
 XX genes from Drosophila and for elucidating cell signalling and cell-cell
 XX interactions -
 XX PS Disclosure; SEQ ID NO 35958; 21pp + Sequence Listing; English.
 XX CC The invention relates to an isolated nucleic acid detection reagent
 XX capable of detecting 1000 or more genes from Drosophila. The invention is
 XX useful in developmental biology and in elucidating cell signalling and
 XX cell-cell interactions in higher eukaryotes for the development of
 XX insecticides, therapeutics and pharmaceutical drugs. The invention
 XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 XX sequences (ABL01840-ABL16175) and the encoded proteins
 XX (ABBS7737-ABBS72072).

XX CC The sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic format directly from WIPO
 XX at ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 138 AA;

Query Match 13.1%; Score 275; DB 22; Length 138;
 Best Local Similarity 46.4%; Pred. No. 2e-19;
 Matches 58; Conservative 17; Mismatches 46; Indels 4; Gaps 2;

Qy 54 VALLDLHNPKDSISIENKVPENCERISQSGDFLRYHYNGTLLDGTLPDSSYSRNRFTDT 113
Db 13 VAASAASDPKVKIGIKRV-ENCTRKAKGDLVHVYRGALQDTEFDSSYSRGTPFSF 70
Qy 114 YIQQYVIPGMDGLGVCIGKRRIVVPHLGYGEGR--GNIPGSALVAFDIHVDPH 171
Db 71 TLGARQVIKWDQGHILGMCGEQORKUTIPPGLGYGASGAGGKIPPNVAVLVDTELKIE 130
Qy 172 NPSDS 176
Db 131 PRSGS 135

Search completed: April 26, 2003, 06:53:07
Job time : 29.2202 secs

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: April 26, 2003, 06:48:54 ; Search time 9.81714 Seconds
(without alignments)
1162.874 Million cell updates/sec

Title: US-09-225-502-8
Perfect score: 2106
Sequence: 1 TYGETGWLIPGMDKGLGMC.....VNDFPLKLLYFTNLNIFVLM 388

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1022	48.5	581	2	US-08-989-386-7
2	1000.5	47.5	582	2	US-08-989-386-1
3	247.5	11.8	141	1	US-07-822-966B-6
4	247.5	11.8	142	1	US-08-336-618-18
5	247.5	11.8	142	5	PCT-US92-03993-7
6	237.5	11.3	135	1	US-08-336-618-20
7	236.5	11.2	141	2	US-08-803-899-6
8	235	11.2	104	3	US-08-894-173-86
9	235	11.0	105	3	US-09-398-193-86
10	232.5	11.0	105	3	US-08-894-173-84
11	232.5	11.0	105	4	US-09-398-193-84
12	218	10.4	99	5	PCT-US92-03993-5
13	208.5	9.9	107	3	US-08-894-173-69
14	208.5	9.9	107	3	US-08-894-173-83
15	208.5	9.9	107	4	US-09-398-193-69
16	208.5	9.9	107	4	US-09-398-193-83
17	208.5	9.9	119	5	PCT-US92-03993-1
18	208.5	9.9	120	1	US-08-336-618-17
19	192	9.1	384	1	US-08-707-793A-5
20	192	9.1	384	1	US-08-707-792A-5
21	189	9.0	458	1	US-08-336-618-24
22	188	8.9	113	5	PCT-US92-03993-4
23	188	8.9	114	1	US-08-336-618-16
24	188	8.9	459	1	US-08-336-618-12
25	188	8.9	459	1	US-08-336-618-26
26	186	8.8	107	3	US-08-894-173-66
27	186	8.8	107	3	US-08-894-173-79

Sequence 66, Appl	28	186	8.8	107	4	US-09-398-193-66
Sequence 79, Appl	29	186	8.8	107	4	US-09-398-193-79
Sequence 2, Appl	30	184.5	8.8	108	2	US-08-803-899-2
Sequence 5, Appl	31	184.5	8.8	108	2	US-08-803-899-5
Sequence 6, Appl	32	184.5	8.8	224	1	US-08-707-793A-6
Sequence 6, Appl	33	184.5	8.8	224	1	US-08-707-792A-6
Sequence 4, Appl	34	184	8.7	378	1	US-08-707-793A-4
Sequence 4, Appl	35	184	8.7	378	1	US-08-707-792A-4
Sequence 2, Appl	36	177	8.4	107	1	US-08-197-795-2
Sequence 15, Appl	37	177	8.4	107	1	US-08-336-618-15
Sequence 3, Appl	38	177	8.4	107	5	PCT-US92-03993-3
Sequence 2, Appl	39	173	8.2	107	1	PCT-US95-01721-2
Sequence 13, Appl	40	173	8.2	107	1	US-08-336-618-13
Sequence 1, Appl	41	173	8.2	107	2	US-08-963-601-1
Sequence 7, Appl	42	173	8.2	107	2	US-08-744-701-7
Sequence 67, Appl	43	173	8.2	107	3	US-08-894-173-67
Sequence 80, Appl	44	173	8.2	107	3	US-08-894-173-80
Sequence 67, Appl	45	173	8.2	107	4	US-09-398-193-67

ALIGNMENTS

RESULT 1
US-08-989-386-7
; Sequence 7, Application US/08989386
; Patent No. 5989860
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN ISOMERASE HOMOLOGS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,386
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0443 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 581 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 894162
US-08-989-386-7

Query Match 48.5%; Score 1022; DB 2; Length 581;
Best Local Similarity 55.8%; Pred. No. 3.8e-100; Indels 20; Gaps 6;
Matches 198; Conservative 58; Mismatches 79; Indels 20; Gaps 6;

Qy 1 TYGIGWLIIPGMDKGLGCMVGEKRIITIPPLAYGEDGDKDIPGQASLVDFVALLDLH 60
Db 202 TYIGSGWLIIPGMDKGLGCMVGEKRIITIPPLAYGEKGYGVIPGQASLVDFVALLDVH 261
Qy 61 NPKDSISTENKVVPCNERISQSGDFURHYNGTLLDGTLPDSSYSRNRTPDTYIGQYV 120
Db 262 NPKDVTQLETLPPGCVRRAGADFMRYHNGSLMDGTLPDSSYSRNRHTYVIGQYI 321
Qy 121 IPGMDGGLGVCIGEKRIIVPPHLYGEBEGRGN-IPGSAVLVDFIHDVDFHNPDSISI 179
Db 322 IPGMDQGLQACIGERRITIPPLAYGENGTDKIPGSAVLVDFVHVIDFHPNPDVVEI 381
Qy 180 TSHYKPPD-CSVLKSGDYLYKHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMDG 238
Db 382 KTLSPENCNETSKIGDFIRHYNCSLLDGTLPDSSHDYEAQBITLGANKVIEGLDRG 441
Qy 239 LREMCVGEKRTVIIPPHLYGEGAGVDGEPGSAVLVDFIELLELVAGLPEGYMFIWNGEV 298
Db 442 LQGMCVGERQLIIPPHLAHENGARG-VPGSAVLVFEVLVSREDGLPTGYLVFYQDP 500
Qy 299 SPNLFEEIN-----KVTFFCCPFVSWRWYPEGRQI-PQDSNDSPADL 342
Db 501 STSLFEDMDLNGKEVPPPEEFSSFIKAQVN-----EGKRLMPGQDPDKTISDM 549

RESULT 2
US-08-989-386-1
; Sequence 1, Application US/08989386
; Patent No. 5989860
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN ISOMERASE HOMOLOGS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-Seq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,386
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0443 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 582 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: OVARUT01
; CLONE: 2255114
; US-08-989-386-1

Query Match 47.5%; Score 1000.5; DB 2; Length 582;
Best Local Similarity 55.1%; Pred. No. 7.5e-98;
Matches 189; Conservative 60; Mismatches 73; Indels 21; Gaps 6;

Qy 1 TYGIGWLIIPGMDKGLGCMVGEKRIITIPPLAYGEDGDKDIPGQASLVDFVALLDLH 60
Db 203 TYIGSGWLIIPGMDKGLGCMVGEKRIITIPPLAYGEKGYGVIPGQASLVDFVALLDVH 262
Qy 61 NPKDSISTENKVVPCNERISQSGDFURHYNGTLLDGTLPDSSYSRNRTPDTYIGQYV 120
Db 263 NPKDAVQLETLPPGCVRRAGADFMRYHNGSLMDGTLPDSSYSRNRHTYVIGQYI 322
Qy 121 IPGMDGGLGVCIGEKRIIVPPHLYGEBEGRGN-IPGSAVLVDFIHDVDFHNPDSISI 179
Db 323 IPGMDQGLQACIGERRITIPPLAYGENGTDKIPGSAVLVDFVHVIDFHPNPDVVEI 382
Qy 180 TSHYKPPD-CSVLKSGDYLYKHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMDG 238
Db 383 RLSRPETCNETYKLGDFVRYHNCSSLLDGTLPDSSHDYEAQBITLGANKVIEGLDTG 442
Qy 239 LREMCVGEKRTVIIPPHLYGEGAGVDGEPGSAVLVDFIELLELVAGLPEGYMFIWNGEV 298
Db 443 LQGMCVGERQLIIPPHLAHENGARG-VPGSAVLVFEVLVSREDGLPTGYLVFWHKDP 501
Qy 299 SPNLFEEIN-----KVTFFCCPFVSWRWYPEGRQI 330
Db 502 PANLFEDMDLNGKEVPPPEEFSTFI-----KAQVSEKGRGL 537

RESULT 3
US-07-822-966B-6
; Sequence 6, Application US/07822966B
; Patent No. 5498597
; GENERAL INFORMATION:
; APPLICANT: Steven J. Burakoff
; APPLICANT: Stuart L. Schreiber
; APPLICANT: Barbara E. Blier
; TITLE OF INVENTION: PKBP-13, AN FK506-BINDING
; TITLE OF INVENTION: IMMUNOPHILIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/822,966B
; FILING DATE: January 17, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Frazer, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00530/052001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 141 amino acids
; TYPE: amino acid

STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-822-966B-6

Query Match 11.8%; Score 247.5; DB 1; Length 141;
Best Local Similarity 47.7%; Pred. No. 1.5e-18;
Matches 51; Conservative 18; Mismatches 35; Indels 3; Gaps 2;

QY 63 KDSISIEKNKVPENCERISQSGDFLRHYNGTLLDGTFLDSSYSRNRFTFTYIGQGVIP 122
DB 29 KLQIGVKKRV--DHCPIKSRKGDVLMHMYTGKLEDGTEFDSLSLPONQPFVSLGTGVV 86
QY 123 GMDGLLGVCIGEKRRIVVPPHLYGGEGR-GNIPGSALVFDIHI 168
DB 87 GWDQGLLGMCEGKRLVIPSELGYGERGAPPKIPGGATLVFEVELL 133

RESULT 4

US-08-336-618-18
Sequence 18, Application US/08336618
Patent No. 5763590
GENERAL INFORMATION:
APPLICANT: Peattie, Debra A.
APPLICANT: Harding, Matthew W.
APPLICANT: Livingston, David J.
TITLE OF INVENTION: ISOLATION OF AN MR 52,000 FK506 BINDING
TITLE OF INVENTION: PROTEIN AND MOLECULAR CLONING OF A CORRESPONDING HUMAN
TITLE OF INVENTION: CDNA
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith and Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,618
FILING DATE: 09-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/963,325
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/777,752
FILING DATE: 11-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 09-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: VP191-06A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-618-18

Query Match 11.8%; Score 247.5; DB 1; Length 142;
Best Local Similarity 47.7%; Pred. No. 1.5e-18;
Matches 51; Conservative 18; Mismatches 35; Indels 3; Gaps 2;

QY 63 KDSISIEKNKVPENCERISQSGDFLRHYNGTLLDGTFLDSSYSRNRFTFTYIGQGVIP 122
DB 30 KLQIGVKKRV--DHCPIKSRKGDVLMHMYTGKLEDGTEFDSLSLPONQPFVSLGTGVV 87
QY 123 GMDGLLGVCIGEKRRIVVPPHLYGGEGR-GNIPGSALVFDIHI 168
DB 88 GWDQGLLGMCEGKRLVIPSELGYGERGAPPKIPGGATLVFEVELL 134

RESULT 5

PCT-US92-03993-7
Sequence 7, Application PC/TUS9203993
GENERAL INFORMATION:
APPLICANT: Harding, Matthew W.
TITLE OF INVENTION: REKBP: A NOVEL PROLYL ISOMERASE AND
TITLE OF INVENTION: RAPAMYCIN/FK506 BINDING PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/03993
FILING DATE: 19920507
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/697,113
FILING DATE: 08-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: VP191-05A PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-03993-7

Query Match 11.8%; Score 247.5; DB 5; Length 142;
Best Local Similarity 47.7%; Pred. No. 1.5e-18;
Matches 51; Conservative 18; Mismatches 35; Indels 3; Gaps 2;

QY 63 KDSISIEKNKVPENCERISQSGDFLRHYNGTLLDGTFLDSSYSRNRFTFTYIGQGVIP 122
DB 30 KLQIGVKKRV--DHCPIKSRKGDVLMHMYTGKLEDGTEFDSLSLPONQPFVSLGTGVV 87
QY 123 GMDGLLGVCIGEKRRIVVPPHLYGGEGR-GNIPGSALVFDIHI 168
DB 88 GWDQGLLGMCEGKRLVIPSELGYGERGAPPKIPGGATLVFEVELL 134

RESULT 6

US-08-336-618-20
Sequence 20, Application US/08336618
Patent No. 5763590
GENERAL INFORMATION:
APPLICANT: Peattie, Debra A.
APPLICANT: Harding, Matthew W.
APPLICANT: Livingston, David J.
TITLE OF INVENTION: ISOLATION OF AN MR 52,000 FK506 BINDING

TITLE OF INVENTION: PROTEIN AND MOLECULAR CLONING OF A CORRESPONDING HUMAN

TITLE OF INVENTION: CDNA

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith and Reynolds, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/336,618

FILING DATE: 09-NOV-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/963,325

FILING DATE: 16-OCT-1992

APPLICATION NUMBER: US 07/777,752

FILING DATE: 11-OCT-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/

FILING DATE: 09-OCT-1992

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: VP191-06A

TELEPHONE: 617-861-6240

TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 135 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-336-618-20

Query Match 11.3%; Score 237.5; DB 1; Length 135;

Best Local Similarity 43.1%; Pred. No. 1.6e-17;

Matches 53; Conservative 22; Mismatches 41; Indels 7; Gaps 3;

QY 49 SLVFDVALLDHPKDSISIEKVVPENCERISQSGDFLRHYNGTLLD-GTLFDSYSR 107

Db 13 STILAGSLSDU-----EIGIKRIPVEDCLIKMPGDKVKVHYTGSLLESGLTVDSSYSR 67

QY 108 NRTDITYGGYVPGMDGLGVCIGEKRRIVVPHLGYGEEG-RGNIPGSALVFDIH 166

Db 68 GSPIAFELGVRVKGWDQGVAGMVCVGEKRLQIPSSLAYGVRGVPVIPSADLVFDE 127

QY 167 VID 169

Db 128 LVD 130

RESULT 7

US-08-803-899-6

Sequence 6, Application US/08803899

Patent No. 5912224

GENERAL INFORMATION:

APPLICANT: DONAHOF, PATRICIA K.

APPLICANT: WANG, TONGWEN

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ENHANCING

CELLULAR RESPONSE TO TGF-BETA LIGANDS

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C

STREET: 1100 NEW YORK AVENUE, SUITE 600

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/803,899

FILING DATE: 02/21/1997

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/012,054

FILING DATE: 02/22/1996

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: STEFFE, ERIC K.

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 0609.4240001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)371-2600

TELEFAX: (202)371-2540

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 141 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-803-899-6

Query Match 11.2%; Score 236.5; DB 2; Length 141;

Best Local Similarity 46.7%; Pred. No. 2.2e-17;

Matches 50; Conservative 18; Mismatches 36; Indels 3; Gaps 2;

QY 63 KDSISIEKVVPENCERISQSGDFLRHYNGTLLDGTFLFDSYSRNRFTDVIYGGYVIP 122

Db 29 KLIQGVKRV--DHCPIKSRKGDVLMHYTKLEDGTEFDSLSLPQNPQFVSLGTGVK 86

QY 123 GMDGLGVCIGEKRRIVVPHLGYGEEG-RGNIPGSALVFDIHVI 168

Db 87 GWDQGLGVCIGEKRRIVVPHLGYGEEG-RGNIPGSALVFDIHVI 133

RESULT 8

US-08-894-173-86

Sequence 86, Application US/08894173A

Patent No. 6090612

GENERAL INFORMATION:

APPLICANT: Medical Research Council

TITLE OF INVENTION: Adenylate cyclase and uses therefor

FILE REFERENCE: P14716C

CURRENT APPLICATION NUMBER: US/08/894,173A

CURRENT FILING DATE: 1997-08-13

NUMBER OF SEQ ID NOS: 97

SOFTWARE: Patent in Ver. 2.1

SEQ ID NO 86

LENGTH: 104

TYPE: PRT

ORGANISM: Yeast

US-08-894-173-86

Query Match 11.2%; Score 235; DB 3; Length 104;

Best Local Similarity 47.9%; Pred. No. 2e-17;

Matches 46; Conservative 16; Mismatches 34; Indels 0; Gaps 0;

QY 187 DCSVLKKGDKYLYKHYNASLLDGLTDLSTWNLGTYNTIVLGSQVVLQMDGLREMCVGE 246

Db 8 DCLIKAMPDKVKVHYTGSLESGTVFDSYSRGSPIAFELGVRVKGWDQGVAGMVCVGE 67

QY 247 KETVLIPPHLGYGEEGVDGVPGSALVFDIHEL 282

Db 68 KRKLQIPSSLAYGERGVGVIPPSADLVDFVDELVDV 103

RESULT 9

US-09-398-193-86
; Sequence 86, Application US/09398193
; Patent No. 6197581
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: Adenylate cyclase and uses therefor
; FILE REFERENCE: P24360-
; CURRENT APPLICATION NUMBER: US/09/398,193
; CURRENT FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Yeast
US-09-398-193-86

Query Match 11.2%; Score 235; DB 4; Length 104;
Best Local Similarity 47.9%; Pred. No. 2e-17;
Matches 46; Conservative 16; Mismatches 34; Indels 0; Gaps 0;

QY 187 DCSVLSKKGDYLYKHYNASILDGTLDDSTWNLGKTYNIVLGSQGVVLGMDGLREMCVGE 246

Db 8 DCLIKAMPQDKVKKVHYTGSLESTGVFDSSYSRGSPIAFELGVRGVIRKQWDQVAGMCVGE 67

QY 247 KRTVIIPPHLYGAGVDEVPGSVAVLVDIELLEL 282

Db 68 KRKLQIPSSLAYGERGVGVIPPSADLVDFVDELVDV 103

RESULT 10

US-08-894-173-84
; Sequence 84, Application US/08894173A
; Patent No. 6090612
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: Adenylate cyclase and uses therefor
; FILE REFERENCE: P14716C
; CURRENT APPLICATION NUMBER: US/08/894,173A
; CURRENT FILING DATE: 1997-08-13
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Human
US-08-894-173-84

Query Match 11.0%; Score 232.5; DB 3; Length 105;
Best Local Similarity 49.5%; Pred. No. 3.7e-17;
Matches 47; Conservative 15; Mismatches 32; Indels 1; Gaps 1;

QY 75 ENCRISQSGDFLRHYNGTLLDGTLDFTDSSYSRNRFTDYIGQYVIPGMDGELGVCIG 134

Db 3 DHCPIKSRKGDVLMHMYTKLEDGTEFDSLPQNPQPFVSLGTGQVIKQWDQGLGMYEG 62

QY 135 EKRRIVPPHLYGGEGR-GNIPGSVAVLVDIHWI 168

Db 63 EKRLVIPSSELGYGERGAPPKIPGGATLVFEVELL 97

RESULT 11

US-09-398-193-84
; Sequence 84, Application US/09398193
; Patent No. 6197581
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: Adenylate cyclase and uses therefor
; FILE REFERENCE: P24360-

; CURRENT APPLICATION NUMBER: US/09/398,193
; CURRENT FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Human
US-09-398-193-84

Query Match 11.0%; Score 232.5; DB 4; Length 105;
Best Local Similarity 49.5%; Pred. No. 3.7e-17;
Matches 47; Conservative 15; Mismatches 32; Indels 1; Gaps 1;

QY 75 ENCRISQSGDFLRHYNGTLLDGTLDFTDSSYSRNRFTDYIGQYVIPGMDGELGVCIG 134

Db 3 DHCPIKSRKGDVLMHMYTKLEDGTEFDSLPQNPQPFVSLGTGQVIKQWDQGLGMYEG 62

QY 135 EKRRIVPPHLYGGEGR-GNIPGSVAVLVDIHWI 168

Db 63 EKRLVIPSSELGYGERGAPPKIPGGATLVFEVELL 97

RESULT 12

PCT-US92-03993-5
; Sequence 5, Application PC/TUS9203993
; GENERAL INFORMATION:
; APPLICANT: Harding, Matthew W.
; TITLE OF INVENTION: RPKBP: A NOVEL PROLYL ISOMERASE AND
; TITLE OF INVENTION: RAPAMYCIN/FK506 BINDING PROTEIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/03993
; FILING DATE: 19920507
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/697,113
; FILING DATE: 08-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: VPI91-05A PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-03993-5

Query Match 10.4%; Score 218; DB 5; Length 99;
Best Local Similarity 49.4%; Pred. No. 1.2e-15;
Matches 44; Conservative 14; Mismatches 29; Indels 2; Gaps 1;

QY 63 KDSISIENKVVPCNERISQSGDFLRHYNGTLLDGTLDFTDSSYSRNRFTDYIGQYVIP 122

Db 8 KLAQIGVKRV--DHCPIKSRKGDVLMHMYTKLEDGTEFDSLPQNPQPFVSLGTGQVIK 65

GenCore version 5.1.4 p5_4578
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OM protein - protein search, using sw model

Run on: April 26, 2003, 06:51:02 ; Search time 12.2714 Seconds
(without alignments)
2533.559 Million cell updates/sec

Title: US-09-225-502-8
Perfect score: 2106
Sequence: 1 TYGEIGWLIPGMDKGLLGMC.....VNDFFLKLLYFTNINLVFLM 388

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 301932 seqs, 80129803 residues

Total number of hits satisfying chosen parameters: 301932

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2106	100.0	388	10	US-09-225-502-8
2	1606	76.3	574	10	US-09-225-502-6
3	1000.5	47.5	434	10	US-09-925-297-808
4	997.5	47.4	441	10	US-09-225-502-4
5	544.5	25.9	366	10	US-09-925-300-1692
6	541.5	25.7	336	10	US-09-225-502-2
7	234.5	11.1	211	9	US-09-978-295A-145
8	234.5	11.1	211	9	US-09-978-697-145
9	234.5	11.1	211	9	US-09-978-192A-145
10	234.5	11.1	211	9	US-09-999-832A-145
11	234.5	11.1	211	9	US-10-001-054-4
12	234.5	11.1	211	9	US-09-978-189-145
13	234.5	11.1	211	9	US-10-028-072-384
14	234.5	11.1	211	9	US-10-121-049-384
15	234.5	11.1	211	9	US-10-123-904-384
16	234.5	11.1	211	9	US-10-140-470-384
17	234.5	11.1	211	9	US-10-175-746-384
18	234.5	11.1	211	9	US-10-176-918-384
19	234.5	11.1	211	9	US-10-176-921-384

20	234.5	11.1	211	9	US-10-137-865-384	Sequence 384, App
21	234.5	11.1	211	9	US-10-140-474-384	Sequence 384, App
22	234.5	11.1	211	9	US-10-142-431-384	Sequence 384, App
23	234.5	11.1	211	9	US-10-143-114-384	Sequence 384, App
24	234.5	11.1	211	9	US-10-140-002-384	Sequence 384, App
25	234.5	11.1	211	9	US-09-978-608A-145	Sequence 145, App
26	234.5	11.1	211	9	US-10-142-419-384	Sequence 384, App
27	234.5	11.1	211	9	US-09-776-724A-189	Sequence 189, App
28	234.5	11.1	211	9	US-09-978-131A-145	Sequence 145, App
29	234.5	11.1	211	9	US-09-978-403A-145	Sequence 145, App
30	234.5	11.1	211	9	US-09-978-564A-145	Sequence 145, App
31	234.5	11.1	211	9	US-09-978-585A-145	Sequence 145, App
32	234.5	11.1	211	9	US-10-017-081A-145	Sequence 145, App
33	234.5	11.1	211	9	US-10-123-262-384	Sequence 384, App
34	234.5	11.1	211	9	US-10-142-423-384	Sequence 145, App
35	234.5	11.1	211	9	US-09-978-824-145	Sequence 145, App
36	234.5	11.1	211	9	US-09-981-915A-145	Sequence 145, App
37	234.5	11.1	211	9	US-09-999-833A-145	Sequence 384, App
38	234.5	11.1	211	9	US-10-121-050-384	Sequence 145, App
39	234.5	11.1	211	9	US-10-141-755-384	Sequence 145, App
40	234.5	11.1	211	9	US-10-167-749-145	Sequence 145, App
41	234.5	11.1	211	9	US-09-918-585A-145	Sequence 384, App
42	234.5	11.1	211	9	US-10-143-032-384	Sequence 145, App
43	234.5	11.1	211	9	US-09-978-423A-145	Sequence 145, App
44	234.5	11.1	211	9	US-10-013-921A-145	Sequence 145, App
45	234.5	11.1	211	9	US-10-123-108-384	Sequence 384, App

ALIGNMENTS

RESULT 1
US-09-225-502-8
; Sequence 8, Application US/09225502A
; Patent No. US20020137127A1
; GENERAL INFORMATION:
; APPLICANT: Moore et al.
; TITLE OF INVENTION: Human FK506 Binding Proteins
; FILE REFERENCE: PF392
; CURRENT APPLICATION NUMBER: US/09/225,502A
; CURRENT FILING DATE: 1999-01-06
; PRIOR APPLICATION NUMBER: 60/070,875
; PRIOR FILING DATE: 1998-01-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-225-502-8

Query Match 100.0%; Score 2106; DB 10; Length 388;
Best Local Similarity 100.0%; Pred. No. 1.4e-188;
Matches 388; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TYGEIGWLIPGMDKGLLGMCVGEKRIITIPFLAYGSDGDKIPGQASLVFDVALLDLH	60
DB	1	TYGEIGWLIPGMDKGLLGMCVGEKRIITIPFLAYGSDGDKIPGQASLVFDVALLDLH	60
QY	61	NPKDSISIEKNKVPENCERISQSGDFLRHYNGTLLDGLTLPDSSYSRNRFTDTYIGQGV	120
DB	61	NPKDSISIEKNKVPENCERISQSGDFLRHYNGTLLDGLTLPDSSYSRNRFTDTYIGQGV	120
QY	121	IPGMDGLGVCIGEKRIIVVPHLGYGEGRGNI PGSAVLVFDHVIDFHNPSDSISIT	180
DB	121	IPGMDGLGVCIGEKRIIVVPHLGYGEGRGNI PGSAVLVFDHVIDFHNPSDSISIT	180
QY	181	SHYKPPDCSVLSKGDYLYKHYNASLLDGLTLDSTNWLKGTNYIVLGSQVVLGMDMGLR	240
DB	181	SHYKPPDCSVLSKGDYLYKHYNASLLDGLTLDSTNWLKGTNYIVLGSQVVLGMDMGLR	240
QY	241	EMCVGEKRIIVPHLGYGEGVDPGSAVLVFDIELLELVAGLPGGYMFINGEVSP	300
DB	241	EMCVGEKRIIVPHLGYGEGVDPGSAVLVFDIELLELVAGLPGGYMFINGEVSP	300

Db 241 EMCVGEKRTVLIIPPHLGYGAGVDGVEPGSAVLVFDIIELELVAGLPEGYMFIWNGEVSP 300
 Qy 301 NLFBEINKVTFCCPFVSWRWYBEGRQQLPQDSNDSPADLIPASWNNHMTATYPLFPN 360
 Db 301 NLFBEINKVTFCCPFVSWRWYBEGRQQLPQDSNDSPADLIPASWNNHMTATYPLFPN 360
 Qy 361 GGGTYPEVVDNFPPLKLLYFTNLNPFVLM 388
 Db 361 GGGTYPEVVDNFPPLKLLYFTNLNPFVLM 388

RESULT 2

US-09-225-502-6
 ; Sequence 6, Application US/09225502A
 ; Patent No. US20020137127A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Moore et al.
 ; TITLE OF INVENTION: Human FK506 Binding Proteins
 ; FILE REFERENCE: PF392
 ; CURRENT APPLICATION NUMBER: US/09/225,502A
 ; CURRENT FILING DATE: 1999-01-06
 ; PRIOR APPLICATION NUMBER: 60/070,875
 ; PRIOR FILING DATE: 1998-01-09
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 574
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-225-502-6

Query Match 76.3%; Score 1606; DB 10; Length 574;
 Best Local Similarity 98.1%; Pred. No. 1.2e-141;
 Matches 302; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TYGEIGWLIIPGMDKGLGMCVGEKRIITIPPLAYGEGDGDGKDIPQASLVFDVALLDLH 60
 Db 195 TVVGIGWLIIPGMDKGLGMCVGEKRIITIPPLAYGEGDGDGKDIPQASLVFDVALLDLH 254
 Qy 61 NPKDSISIEKVVPCNERISQSGDFLYHYNGTLLDGTLPDSSYSRNRTPDTYIGQGV 120
 Db 255 NPKDSISIEKVVPCNERISQSGDFLYHYNGTLLDGTLPDSSYSRNRTPDTYIGQGV 314
 Qy 121 IPGMDGGLGVCIGEKRRIVVPHLGYGEGRGNIPGSVAVLFDIIELELVAGLPEGYMFIWNGEVSP 180
 Db 315 IPGMDGGLGVCIGEKRRIVVPHLGYGEGRGNIPGSVAVLFDIIELELVAGLPEGYMFIWNGEVSP 374
 Qy 181 SHYKPPDCSVLSKGGDYLYKHYNASILLDGTLLDSTWNLGKTYNIVLGSQVVLGMDMGLR 240
 Db 375 SHYKPPDCSVLSKGGDYLYKHYNASILLDGTLLDSTWNLGKTYNIVLGSQVVLGMDMGLR 434
 Qy 241 EMCVGEKRTVLIIPPHLGYGAGVDGVEPGSAVLVFDIIELELVAGLPEGYMFIWNGEVSP 300
 Db 435 EMCVGEKRTVLIIPPHLGYGAGVDGVEPGSAVLVFDIIELELVAGLPEGYMFIWNGEVSP 494
 Qy 301 NLFBEINK 308
 Db 495 NLFBEIDK 502

RESULT 3

US-09-225-297-808
 ; Sequence 808, Application US/09925297
 ; Patent No. US20020081659A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA105
 ; CURRENT APPLICATION NUMBER: US/09/225,297
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05989
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270

; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 928
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 808
 ; LENGTH: 434
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-225-297-808

Query Match 47.5%; Score 1000.5; DB 10; Length 434;
 Best Local Similarity 55.1%; Pred. No. 3e-85;
 Matches 189; Conservative 60; Mismatches 73; Indels 21; Gaps 6;

Qy 1 TYGEIGWLIIPGMDKGLGMCVGEKRIITIPPLAYGEGDGDGKDIPQASLVFDVALLDLH 60
 Db 55 TYVGSWLIKGMDOGLGMCPEGRKIIIPFLAYGEGYGTVPQASLVFVLLIDVH 114
 Qy 61 NPKDSISIEKVVPCNERISQSGDFLYHYNGTLLDGTLPDSSYSRNRTPDTYIGQGV 120
 Db 115 NPKDAVQLELLELPVCGVRRAGAGDFMYHYNGSLMDGTLPDSSYSRNRHTYNTYIGQYI 174
 Qy 121 IPGMDGGLGVCIGEKRRIVVPHLGYGEGRGNIPGSVAVLFDIIELELVAGLPEGYMFIWNGEVSP 179
 Db 175 IPGMDGGLGVCIGEKRRIVVPHLGYGEGRGNIPGSVAVLFDIIELELVAGLPEGYMFIWNGEVSP 234
 Qy 180 TSHYKPPD-CVLSKGGDYLYKHYNASILLDGTLLDSTWNLGKTYNIVLGSQVVLGMDMG 238
 Db 235 RTLSRPSETCNETTKLGDVRYHYNCSSLDDGTQLFTSHDYGAQPEATLGANKVIEGLDTG 294
 Qy 239 LREMCVGEKRTVLIIPPHLGYGAGVDGVEPGSAVLVFDIIELELVAGLPEGYMFIWNGEVSP 298
 Db 295 LQMCVGERQLIVPPLAHGESGARG-VFGSAVLFEVLVSREDGLPTGYLFWHNDP 353
 Qy 299 SPNIFE-EINK-----VTFPCPFVSWRWYBEGRQQL 330
 Db 354 PANLFEDMDLNKDGVEPPEPFTFI-----KAQVSEKGR 389

RESULT 4

US-09-225-502-4
 ; Sequence 4, Application US/09225502A
 ; Patent No. US20020137127A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Moore et al.
 ; TITLE OF INVENTION: Human FK506 Binding Proteins
 ; FILE REFERENCE: PF392
 ; CURRENT APPLICATION NUMBER: US/09/225,502A
 ; CURRENT FILING DATE: 1999-01-06
 ; PRIOR APPLICATION NUMBER: 60/070,875
 ; PRIOR FILING DATE: 1998-01-09
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 441
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-225-502-4

Query Match 47.4%; Score 997.5; DB 10; Length 441;
 Best Local Similarity 55.1%; Pred. No. 5.9e-85;
 Matches 189; Conservative 59; Mismatches 74; Indels 21; Gaps 6;

Qy 1 TYGEIGWLIIPGMDKGLGMCVGEKRIITIPPLAYGEGDGDGKDIPQASLVFDVALLDLH 60
 Db 62 TYVGSWLIKGMDOGLGMCPEGRKIIIPFLAYGEGYGTVPQASLVFVLLIDVH 121
 Qy 61 NPKDSISIEKVVPCNERISQSGDFLYHYNGTLLDGTLPDSSYSRNRTPDTYIGQGV 120
 Db 122 NPKDAVQLELLELPVCGVRRAGAGDFMYHYNGSLMDGTLPDSSYSRNRHTYNTYIGQYI 181
 Qy 121 IPGMDGGLGVCIGEKRRIVVPHLGYGEGRGNIPGSVAVLFDIIELELVAGLPEGYMFIWNGEVSP 179
 Db 182 IPGMDGGLGVCIGEKRRIVVPHLGYGEGRGNIPGSVAVLFDIIELELVAGLPEGYMFIWNGEVSP 241

QY 180 TSHYKPPD-CSVLSKGGDYLYKHYNASLLDGTLLDSTWNLGKTYNIVLGSQVVLGMDMG 238
DB 242 RTLSRPSCTNCTYGLGDFVRYHNCSLDGTQLFTSHDYGAQOEAATLGANKVIEGLDTG 301
QY 239 LREMCVGEKRTVIIPHLGGEAGVDCGVEGSAVLVDFDIELLELVAAGLPEGYMEIWNAGEV 298
DB 302 LQCMCGERRQLIVPPLAHGEGSARG-VFGSAVLLFEVELVSREDGLPTGYLFWHKDP 360
QY 299 SPNLFBEI--NK-----VTFPCPFVSWRRWYPEGKQL 330
DB 361 PANLFEDIDLKDGVEPPEBFSTFI-----KAQVSEKGR 396

RESULT 5

US-09-925-300-1692
; Sequence 1692, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1692
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1692

Query Match 25.9%; Score 544.5; DB 10; Length 366;
Best Local Similarity 48.5%; Pred. No. 9.5e-43;
Matches 98; Conservative 37; Mismatches 66; Indels 1; Gaps 1;

QY 62 PKDSISIEKVVPCNERISQSGDFLRHYHNGTLLDGTLPDSSYSRNRFTFYIGQGYI 121
DB 76 PLEDVIERHYHIPRACPREVQMGDFVRYHNGTFEDGKKFDSYDRNTLVAIVVGVRLLI 135
QY 122 PGMDEGLLVCIGKRRIVVPHLGYGEG-RGNIPGSAVLVDFDTHVDFHNPDSISIT 180
DB 136 TGMDRGLMGCMVNERLLIVPHLGYGIGLAGLIPDPTLYFDVVLVDVWKNEDTVQVS 195
QY 181 SHYKPPDCSVLSKGGDYLYKHYNASLLDGTLLDSTWNLGKTYNIVLGSQVVLGMDMGLR 240
DB 196 TLLRPPHCPRMVQDGFVRYHNGTLLDGTSPDTSYSGKGTDTYVVGSGWLKMGMDQGLL 255
QY 241 EMCVGEKRTVIIPHLGGEAG 262
DB 256 GMCPCGRRKIIIPPLAYGEGK 277

RESULT 6

US-09-225-502-2
; Sequence 2, Application US/09225502A
; Patent No. US20020137127A1
; GENERAL INFORMATION:
; APPLICANT: Moore et al.
; TITLE OF INVENTION: Human FK506 Binding Proteins
; FILE REFERENCE: PF392
; CURRENT APPLICATION NUMBER: US/09/225,502A
; CURRENT FILING DATE: 1999-01-06
; PRIOR APPLICATION NUMBER: 60/070,875

; PRIOR FILING DATE: 1998-01-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-225-502-2

Query Match 25.7%; Score 541.5; DB 10; Length 336;
Best Local Similarity 48.0%; Pred. No. 1.6e-42;
Matches 97; Conservative 38; Mismatches 66; Indels 1; Gaps 1;
QY 62 PKDSISIEKVVPCNERISQSGDFLRHYHNGTLLDGTLPDSSYSRNRFTFYIGQGYI 121
DB 40 PLEDVIERHYHIPRACPREVQMGDFVRYHNGTFEDGKKFDSYDRNTLVAIVVGVRLLI 99
QY 122 PGMDEGLLVCIGKRRIVVPHLGYGEG-RGNIPGSAVLVDFDTHVDFHNPDSISIT 180
DB 100 TGMDRGLMGCMVNERLLIVPHLGYGIGLAGLIPDPTLYFDVVLVDVWKNEDTVQVS 159
QY 181 SHYKPPDCSVLSKGGDYLYKHYNASLLDGTLLDSTWNLGKTYNIVLGSQVVLGMDMGLR 240
DB 160 TLLRPPHCPRMVQDGFVRYHNGTLLDGTSPDTSYSGKGTDTYVVGSGWLKMGMDQGLL 219
QY 241 EMCVGEKRTVIIPHLGGEAG 262
DB 220 GMCPCGRRKIIIPPLAYGEGK 241

RESULT 7

US-09-978-295A-145
; Sequence 145, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03

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; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 11.1%; Score 234.5; DB 9; Length 211;

Best Local Similarity 36.8%; Pred. No. 4e-14;

Matches 46; Conservative 29; Mismatches 47; Indels 3; Gaps 2;

QY 51 VEDVALLDHNPKDSISIEKNVVPENCERISQSGDFLRYHYNGTL-LDGTLPDSSYSRNR 109

Db 12 LFTVSLGALIPPEVKVLELQKRFCHRTKTKGGDMLVHYEGYDEKDGSLFHSHTKHNN 71

QY 110 TPTYIQGGYV-IPGMDGELGVCIGEKRRIVVPPHLYGEGRGNIPGSAVLVFDIHV 167

Db 72 GQPIWFTLGILEALKGWDQGLKGMVGEKRLIIPPALGYGKGKGPPESTLIFNIDL 131

QY 168 IDFNH 172

Db 132 LEIRN 136

RESULT 8

US-09-978-697-145

; Sequence 145, Application US/09978697

; Patent No. US20020169284A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Deenoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

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; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2630P1C27

; CURRENT APPLICATION NUMBER: US/09/978,697

; CURRENT FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/064249

; PRIOR FILING DATE: 1997-11-03
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; PRIOR FILING DATE: 1997-11-13
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 11.1%; Score 234.5; DB 9; Length 211;

Best Local Similarity 36.8%; Pred. No. 46-14; Indels 3; Gaps 2;
Matches 46; Conservative 29; Mismatches 47;

Qy 51 VDVALLDHPKDSISIEHKVVPENCERISQSGDPLRYHYNGTL-LDGTLPDSSYSRNR 109

Db 12 LFTVSLGALIPPEVKIEVLQKPFCHKTKGGDLMLVHYEGYLEKQSLFHTSKHNN 71

Qy 110 TFDYIGQGV--IFGMEGLLCVIGEKRRIVPPHLYGEGEGRNIPGSAVLVFDIHV 167

Db 72 GQPIWFTILGLEALKGWDQGLKGMVGEKKLIIPALGYGKEGKIPPESTLIFNIDL 131

Qy 168 IDFNH 172

Db 132 LEIRN 136

RESULT 9

US-09-978-192A-145
; Sequence 145, Application US/09978192A

; Patent No. US20020177553A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

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; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tamas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2630P1C9

; CURRENT APPLICATION NUMBER: US/09/978,192A

; CURRENT FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 11.1%; Score 234.5; DB 9; Length 211;
Best Local Similarity 36.8%; Pred. No. 4e-14;
Matches 46; Conservative 29; Mismatches 47; Indels 3; Gaps 2;

QY 51 VFDVALLDHPKDSISIEHKVVPENCERISQSGDFLRVHYNGTL-LDGTLPDSSYSRNR 109
Db 12 LPTVSLIGALPEPEVKVLQKPFCHRTKTKGDLMLVHYEGYLEKQSLPHSTHKNN 71

QY 110 TFDTVIGQYV--IPGMEGLGVCIGEKRIIVPPHLYGEGEGNIPGSAVLVFDIHV 167
Db 72 GQPIWFTLGILEALKGWQGLKGMVCEKRLIIPALGYGKGGKIPPESTLFIENIDL 131

QY 168 IDFNH 172
Db 132 LEIRN 136

RESULT 10
US-09-999-832A-145
; Sequence 145, Application US/0999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC63
; CURRENT APPLICATION NUMBER: US/09/999,832A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250

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US-10-001-054-4

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QY 168 IDFNH 172
Db 132 LEIRN 136

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; Sequence 145, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
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; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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; Publication No. US20030004311A1
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; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang
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(without alignments)
3039.596 Million cell updates/sec

Title: US-09-225-502-8
Perfect score: 2106
Sequence: 1 TYGETGWLIPGMDKGLGMC.....VNDFPLKLLYFTNLNYPVLM 388

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 73:*
1: Piri:*
2: Piri2:*
3: Piri3:*
4: Piri4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1022	48.5	581	2 149669	FKBP65 binding pro
2	572.5	27.2	262	2 T42709	hypothetical prote
3	353.5	16.8	261	2 T31741	hypothetical prote
4	344	16.3	264	2 T29780	hypothetical prote
5	301.5	14.3	259	2 T27586	hypothetical prote
6	286.5	13.6	139	2 T21882	hypothetical prote
7	283.5	13.5	559	1 S55383	peptidylprolyl iso
8	273.5	13.0	241	2 E89251	protein ZC455.10
9	269.5	12.8	311	1 S46228	peptidylprolyl iso
10	265.5	12.6	163	2 T12090	probable peptidylp
11	262	12.4	304	2 T26538	probable peptidylp
12	259	12.3	146	1 S71237	hypothetical prote
13	256.5	12.2	134	1 J70748	probable peptidylp
14	251.5	11.9	551	1 S72485	peptidylprolyl iso
15	251	11.9	140	2 T49668	binding protein -
16	250.5	11.9	568	2 T06489	probable peptidylp
17	247.5	11.8	142	2 JCL365	FK506/rapamycin-bi
18	237.5	11.3	135	2 S25337	peptidylprolyl iso
19	214.5	10.2	113	2 A83180	probable peptidyl-
20	211.5	10.0	165	2 A81878	FKBP-type peptidyl
21	208.5	9.9	120	2 S11090	FK506-binding prot
22	207.5	9.9	152	2 B75347	peptidyl-prolyl ci
23	198.5	9.4	201	1 S75144	FKBP-type peptidyl
24	198	9.4	290	2 T26537	hypothetical prote
25	196	9.3	157	2 C82431	peptidyl-prolyl ci
26	194	9.2	457	2 JC5422	FK506-binding prot
27	191	9.1	259	2 D82331	peptidyl-prolyl ci
28	189	9.0	458	1 A42386	hsp 90-binding pro

30	188	8.9	114	2 A33146	peptidylprolyl iso
31	188	8.9	459	2 A46372	immunophilin FKBP5
32	184.5	8.8	108	2 S54139	FK506-binding prote
33	183	8.7	431	2 T21594	hypothetical prote
34	182	8.6	112	2 T40724	peptidyl-prolyl ci
35	179	8.5	206	2 A80429	peptidylprolyl iso
36	178	8.5	108	2 T26539	hypothetical prote
37	177	8.4	107	2 A61431	peptidylprolyl iso
38	176	8.4	241	2 A64155	hypothetical prote
39	175	8.3	205	2 F83075	peptidyl-prolyl ci
40	175	8.3	458	2 JN0873	immunophilin p59 -
41	174.5	8.3	105	2 A40211	FK506-inhibitable
42	173	8.2	108	2 A35780	peptidylprolyl iso
43	173	8.2	108	2 A42657	FK506-binding prot
44	171.5	8.1	109	2 E82022	peptidylprolyl iso
45	171.5	8.1	270	2 F91153	FKBP-type peptidyl

ALIGNMENTS

RESULT 1

I49669

FKBP65 binding protein - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999

C:Accession: I49669

R:Simsek, S.L.; Kozak, C.A.; Winterstein, D.; Hegamyer, G.; Colburn, N.H.

Genomics 18, 407-409, 1993

A:Title: Sequence and localization of a novel FK506-binding protein to mouse chromosomes

A:Reference number: A48920; MUID:94117013; PMID:7507077

A:Accession: I49669

A:Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-581 <RES>

A:Cross-references: GB:L07063; NID:G894161; PIDN:AAC37678.1; PID:G894162

F:61-108/Domain: BKBP-type peptidylprolyl isomerase homology

F:173-220/Domain: BKBP-type peptidylprolyl isomerase homology <PPI1>

F:285-332/Domain: BKBP-type peptidylprolyl isomerase homology <PPI2>

F:398-445/Domain: BKBP-type peptidylprolyl isomerase homology <PPI4>

Query Match 48.5%; Score 1022; DB 2; Length 581;
Best Local Similarity 55.8%; Pred. No. 2.5e-76;
Matches 198; Conservative 58; Mismatches 79; Indels 20; Gaps 6;

QY	1	TYGEIGWLIPGMDKGLGMCVGEKRIITPPFLAYGSDGDKDIPGQASLVDFVALLDLH	60
DB	202	TVIGSCWLKGMQGLGMCPEKRIIIPFLAYGKGYGTVPQASLVFVLLLDVH	261
QY	61	NPKDSISIKVVPENCERISQSGDFLRHYHNGTLLDGTLDSSYSRNPFTDTIGQYV	120
DB	262	NPKDTVQLETLPPQGVCRRAVAGDFMRHYHNGSLMDGTLDSSYSRNTYTVGQYI	321
QY	121	IPGMDSGLGVCVCEKRIIVPHLGVGEGRGN-IPGSVAVLFDIHDVPHNPSDTSI	179
DB	322	IPGMDQLQACLGERRITVPHLAYGNGTGDKIPGSVAVLFDVHVIDFHNPSDPVEI	381
QY	180	TSHYKPPD-CSVLKSKGDYLYKHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMDMG	238
DB	382	KTLSPREPCNETSKIGDFIRHYHNGSLDGTLLFSSHDEYEAQOEITLGANKVIEGLDRG	441
QY	239	LREMCVGEKRTVIIPHLGVGEAGVDEPGSVAVLFDIELLELVLVAGLPEGYMIWNGEV	298
DB	442	LQMGCVGERQLIVPPLAHGANGARG-VPGSAVLLFEVELSVREDELPTGYLFWYQDP	500
QY	299	SPNLFREIN-----KVTFPCPFVSWRRWYPEGRGQL-PQDSNDSPPADL	342
DB	501	STSLFEDMDLNKDGVEPPPEFSSFIKAQVN-----EGKRLMEGQDPDKTISDM	549

RESULT 2

T42709

[illegible]

Db **I**ntron V 130

RESULT 14
J**T**O748 FK506-binding protein - Botryllus schlosseri
C/Species: Botryllus schlosseri
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
A/Accession: JJT0748; S40074
R;Pancer, Z.; Gershon, H.; Rinkevich, B.
Biochem. Biophys. Res. Commun. 197, 973-977, 1993
A/Title: cDNA cloning of a putative protochordate FK506-binding protein.
A/Reference number: JJT0748; PMID:94092189; PMID:7505578
A/Accession: JJT0748
A/Molecule type: mRNA
A/Residues: 1-134 <**PAN**>
A/Cross-references: EMBL:X76006; NID:g435470; PIDN:CXA53594.1; PID:g435471
C/Superfamily: BKBP-type peptidyprolyl isomerase; BKBP-type peptidyprolyl isomerases
F;41-88/D**a**in: BKBP-type peptidyprolyl isomerase homology <**PPI**>

Query Match 12.2%; Score 256.5; D*B* 1; Length 134;
Best Local Similarity 52.7%; Pred. No. 4.8e-14;
Matches 49; Conservative 15; Mismatches 28; Indels 1; Gaps 1;

QY 77 CERISQSGDFLRHYNGTLTDGTLFDSSYSRNRFTDTYGQGYVPGMDGLLGVCIGEK 136
||||| :||| ||| |::| ::| :||| ||| :||| :||| :||| :||| :||| :

Db 34 CERSKGSVDLDHMYHTLTEDGSKFDSRRDTPFTFLGGYVIKGWDKLLGWCEGER 93
||||| :||| ||| |::| ::| :||| ||| :||| :||| :||| :||| :||| :

QY 137 RRIIVPHLGVGEGR-GNIIPGSALVFDPDHVI 168
:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :

Db 94 RLKLPSDMGYDRGPSPPKIPGGATLIFFDVELL 126
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :

RESULT 15
SZ2485 peptidyprolyl isomerase (**EC** 5.2.1.8) RO*P*i - Arabidopsis thaliana
N/**A**lternate names: FK506-binding protein; immunophilin; rotamase
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
A/Accession: SZ2485; SZ2484
R;Vuicich, V.A.; Gasser, C.S.
Mol. Gen. Genet. 252, 510-517, 1996
A/Title: Novel structure of a high molecular weight FK506 binding protein from Arabi
A/Reference number: SZ2484; MUID:I7071666; PMID:8914512
A/Accession: SZ2485
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-551 <**VUC**>
A/Cross-references: EMBL:U57838; NID:g1373395; PIDN:AAB82062.1; PID:gl373396
A/Note: The nucleotide sequence was submitted to the EMBL Data Library, May 1996
A/Accession: SZ2484
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-429, '**V**', 431-551 <**VUM**>
A/Cross-references: EMBL:U49453; NID:g1354206; PIDN:AAB82061.1; PID:gl354207
C/Genetics:
A/Gene: RO*P*i
A/Introns: 62/1; 91/1; 178/1; 203/1; 295/1; 326/1; 384/3; 425/3; 474/3; 517/2
C/Superfamily: peptidyprolyl isomerase RO*P*i; BKBP-type peptidyprolyl isomerase hom
C/Keywords: calmodulin binding; cis-trans-isomerase
F;57-104/**D**oain: BKBP-type peptidyprolyl isomerase homology <**PPI**1>
F;173-216/**D**oain: BKBP-type peptidyprolyl isomerase homology <**PPI**2>
F;290-339/**D**oain: BKBP-type peptidyprolyl isomerase homology <**PPI**3>
F;414-447/**D**oain: tetratricopeptide repeat homology <**TR**1>
F;449-482/**D**oain: tetratricopeptide repeat homology <**TR**2>
F;483-516/**D**oain: tetratricopeptide repeat homology <**TR**3>
F;529-546/**R**eio: calmodulin-binding #status predicted

Query Match 11.9%; Score 251.5; D*B* 1; Length 551;
Best Local Similarity 30.9%; Pred. No. 8.9e-13;
Matches 71; Conservative 34; Mismatches 88; Indels 37; Gaps 7;

QY 69 ENKVVPENCERISQGDFRLRYHNTGLDGTLPDSSYSRNRTFTDTYGQYVIPGMDEGL 128

Db 49 EGVETPEN-----GDEVEVHYTGTLDDGTGKFDSSRRDRATEFFKFTLGQSQVKGWDIGI 101
Qy 129 LGVCIGEKRRIVPPHLYGEEGR-GNIPGSAVLVFDIHVIDFHNPSD-----SI 177
Db 102 KTMKKGGENAVFTIPAELAYGESGSPPTIPANATLQFDVELLKWDSVKDICKDGGVFKIL 161
Qy 178 SITSHYKPPDCSVLSKKGDYLYKHYNASLLDGTLLDSTWNLGKTYNI--VLGSGQVVLCM 235
Db 162 AVGEKWENP-----KDLDEVLVTFEAKLEDGTV-----VGKSDGVFTVKDGHFPCPAL 209
Qy 236 DMGLREMCVGEKRTVIIPPHLYGEAGV-----DGEVPGSAVLVFDIELL 280
Db 210 TKAVKTMKGEKVLLTVKPOYGFGEKGPASAGEGAVPPNATLEINLELV 259

Search completed: April 26, 2003, 06:50:56
Job time : 13.2714 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 26, 2003, 06:48:55 ; Search time 6.91662 Seconds

(without alignment)
2326.688 Million cell updates/sec

Title: US-09-225-502-8

Perfect score: 2106

Sequence: 1 TYGEICGLIPGMDKGLGMC.....VNDPFLKLYFTNLNYFVLM 388

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1022	48.5	581	1 FKBP_MOUSE	Q61576 mus musculus
2	283.5	13.5	559	1 FKBP_WHEAT	Q43207 triticum ae
3	251	11.9	140	1 FKBP_MOUSE	P45878 mus musculus
4	237.5	11.3	135	1 FKBP_YEAST	P32472 saccharomyc
5	236.5	11.2	141	1 FKBP_HUMAN	P26885 homo sapien
6	233.5	11.1	217	1 FKBP_NEUCR	O60046 neurospora
7	208.5	9.9	120	1 FKBP_MOUSE	P20080 neurospora
8	195	9.3	456	1 FKBP_MOUSE	Q64378 mus musculus
9	194	9.2	457	1 FKBP_MOUSE	Q13451 h 51 kda fk
10	193	9.2	208	1 FKBP_ARATH	Q98cy2 arabidopsis
11	190	9.0	268	1 FKBP_AERHY	O08437 aeromonas h
12	189	9.0	457	1 FKBP_RABIT	P21224 oryctolagus
13	188	8.9	114	1 FKBP_YEAST	P20081 saccharomyc
14	188	8.9	458	1 FKBP_HUMAN	Q02790 homo sapien
15	184.5	8.8	108	1 FKBP_DROME	P48375 drosophila
16	182	8.6	112	1 FKBP_SCHPO	O42993 schizosacch
17	177	8.4	107	1 FKBP_BOVIN	P18203 bos taurus
18	176	8.4	241	1 FKBP_HAEIN	P44760 haemophilus
19	175	8.3	457	1 FKBP_MOUSE	P30416 mus musculus
20	173	8.2	107	1 FKBP_HUMAN	P20071 homo sapien
21	172	8.2	107	1 FKBP_RAT	Q62658 rattus norv
22	171.5	8.1	109	1 FKBP_NEIMA	P56989 neisseria m
23	171.5	8.1	270	1 FKBP_ECOLI	P45523 escherichia
24	169.5	8.0	109	1 FKBP_NEIMB	P25138 neisseria m
25	169	8.0	107	1 FKBP_MOUSE	P26883 mus musculus
26	164.5	7.8	205	1 FKBP_ECOLI	P39311 escherichia
27	164	7.8	241	1 FKBP_BUCAL	P57599 buchnera ap
28	161	7.6	107	1 FKBP_XENLA	O42123 xenopus lae
29	161	7.6	107	1 FKBP_RAT	P97534 rattus norv
30	161	7.6	224	1 FKBP_BOVIN	P26884 bos taurus
31	161	7.6	411	1 FKBP_YEAST	P38911 saccharomyc
32	160.5	7.6	224	1 FKBP_MOUSE	Q22446 mus musculus
33	160	7.6	107	1 FKBP_HUMAN	Q16645 homo sapien

34	159	7.5	223	1 FKBP_RABIT	O46638 oryctolagus
35	159	7.5	224	1 FKBP_HUMAN	Q00688 homo sapien
36	152.5	7.2	124	1 FKBP_STRCH	P28725 streptomyce
37	150.5	7.1	392	1 FKBP_YEAST	Q06205 saccharomyc
38	150	7.1	243	1 MIP_CHLTR	P26623 chlamydia t
39	146	6.9	357	1 FKBP_DROME	P54397 drosophila
40	144.5	6.9	124	1 FKBP_CANAL	P28870 candida alb
41	135.5	6.4	361	1 FKBP_SCHPO	O74191 schizosacch
42	135	6.4	258	1 MIP_CHLPN	Q92703 chlamydia p
43	133	6.3	118	1 FKBP_CORGL	P42458 corynebacte
44	131	6.2	412	1 FKBP_SPOFR	Q26486 spooptera
45	128	6.1	243	1 MIP_CHLMU	O9pjkl chlamydia m

ALIGNMENTS

RESULT 1
FKBP_MOUSE
ID FKBP_MOUSE STANDARD; PRT; 581 AA.
AC Q61576;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 65 kDa FK506-binding protein precursor (EC 5.2.1.8) (FKBP65) (FKBPRP)
DE (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase)
DE (Immunophilin FKBP65).
GN FKBP6 OR FKBP1-RS OR FKBP-RS OR FKBP-RP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JUB6; TISSUE=Epidermis;
RX MEDLINE=94117013; PubMed=7507077;
RA Simek S.L., Kozak C.A., Winterstein D., Hegamyer G., Colburn N.H.;
RT "Sequence and localization of a novel FK506-binding protein to mouse
chromosome 11";
RL Genomics 18:407-409(1993).

[2]
SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLINE=96094328; PubMed=7493967;
RA Coss M.C., Winterstein D., Sowder R.C. II, Simek S.L.;
RT "Molecular cloning, DNA sequence analysis, and biochemical
characterization of a novel 65-kDa FK506-binding protein (FKBP65).";
J. Biol. Chem. 270:29336-29341(1995).
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS DURING
PROTEIN SYNTHESIS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- ENZYME REGULATION: INHIBITED BY BOTH FK506 AND RAPAMYCIN, BUT NOT
BY CYCLOSPORINE A.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM (POTENTIAL).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE LUNG, SPLEEN, HEART, BRAIN
AND TESTIS.
CC -!- PTM: GLYCOSYLATED AND PHOSPHORYLATED.
CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS 4
FKBP-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L07063; AAC37678.1; --
CC HSSP; P20081; 1YAT.
CC MGD; MGI:104769; FKBP6.
CC InterPro; IPR002048; EF-hand.

```

DR InterPro: IPR000886; ER target.
DR InterPro: IPR001179; FKBP_PPIase.
DR Pfam: PF00036; ehfand; 2.
DR Pfam: PF00254; FKBP; 4.
DR SMART: SM00054; EFN; 2.
DR PROSITE: PS00453; FKBP_PPIASE 1; FALSE_NEG.
DR PROSITE: PS00454; FKBP_PPIASE 2; 1.
DR PROSITE: PS00059; FKBP_PPIASE 3; 4.
DR PROSITE: PS00014; ER_TARGET; 1.
DR PROSITE: PS00018; EF_HAND; 1.
KW Isomerase; Rotamase; Repeat; Glycoprotein; Signal; Phosphorylation;
KW Endoplasmic reticulum; Calcium-binding.
FT SIGNAL 1 33
FT CHAIN 34 581
FT DOMAIN 54 146
FT DOMAIN 179 258
FT DOMAIN 291 370
FT DOMAIN 389 482
FT CA_BIND 509 520
FT CA_BIND 554 565
FT CARBOHYD 69 69
FT CARBOHYD 181 181
FT CARBOHYD 293 293
FT CARBOHYD 309 309
FT CARBOHYD 351 351
FT CARBOHYD 392 392
FT CARBOHYD 406 406
FT SITE 578 581
SQ SEQUENCE 581 AA; 64669 MW; 1B51B3032089F555 CRC64;

Query Match 48.5%; Score 1022; DB 1; Length 581;
Best Local Similarity 55.8%; Pred. No. 3.1e-78;
Matches 198; Conservative 58; Mismatches 79; Indels 20; Gaps 6;

QY 1 TYGEIGWLLIPGMDKGLGCMVGEKRIITIPFLAYGDEGDKDIPQASLVFDVALLDLH 60
Db 202 TYGSGWLLKGMDOGLGCMVGEKRIITIPFLAYGDEGDKDIPQASLVFDVALLDLH 261
QY 61 NPKDLSIENKVVENCERISQSGDFLRHYNGTLLDGLTFDSSYSNRRTFTDVIQGYV 120
Db 262 NPKDTVQLETLELPQGVRRVAVGDFWRHYNGSLMDGLTFDSSYSNRHNTIVVGQYI 321
QY 121 IPGMDGLGVCIGEKRIIVVPHLGYGEGRGN-IPGSVAVLFDIHDVFNHPSDSISI 179
Db 322 IPGMDQGLQACIGERRRITVPFLAYGNGTGDKIIPGSVAVLFDVHVDHFNPSDPVEI 381
QY 180 TSHYKPPD-CVLSKKGDYLYKHYNASLLDGLTLLDSTWNLGKTYNIVLGSQVVLGMDMG 238
Db 382 KTLRSPENCNETSKIGDFIRYHNCSLDGLTRFLSSHDEYEAPOEITLGANKVIEGLDRG 441
QY 239 LREMCMVGEKRTVIIPPHLGYGEAGVGEVPGSAVLVFDIBELLEVLVAGLPFGYFIWNGEV 298
Db 442 LQCMCVGERRLVPPHLAHGANGARG-VPGSAVLVFEVLVREDGLPTGYLFWVTQDP 500
QY 299 SPNLFEIN-----KVTFFCPCFVSWRRWYPPGRQL-PQDSNDSPPADL 342
Db 501 STSLFEDMDLNKDGVPPEFFSFIFKAQVN-----EGKRLMPGQDPDKTISDM 549

RESULT 2
FKB7 WHEAT
ID FKB7 WHEAT STANDARD; PRT; 559 AA.
AC Q43207;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 70 kDa peptidylprolyl isomerase (EC 5.2.1.8) (Peptidylprolyl cis-trans
DE isomerase) (Cyclophilin) (PPIase).
GN FKB70.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Triticum.

```

```

OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. ATIR; TISSUE=Root tip;
RA Oshra B., Breiman A.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBSJ databases.
CC -1- FUNCTION: PPIASE THAT BINDS CALMODULIN.
CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS 3
CC FKBP-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 3 TPR REPEATS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X86903; CAA60505.1; -.
CC HSSP; P27124; 1ROT.
CC InterPro: IPR001179; FKBP_PPIase.
CC InterPro: IPR001440; TPR.
CC Pfam; PF00254; FKBP; 3.
CC Pfam; PF00515; TPR; 3.
CC SMART; SM00028; TPR; 3.
CC PROSITE; PS00453; FKBP_PPIASE 1; 1.
CC PROSITE; PS00454; FKBP_PPIASE 2; 3.
CC PROSITE; PS00059; FKBP_PPIASE 3; 3.
KW Isomerase; Rotamase; Repeat; TPR repeat; Heat shock;
KW Calmodulin-binding.
FT DOMAIN 60 148
FT DOMAIN 176 265
FT DOMAIN 293 384
FT REPEAT 401 434
FT REPEAT 450 483
FT REPEAT 484 517
FT REPEAT 517 517
SQ SEQUENCE 559 AA; 62056 MW; 5C5DAE70D716B541 CRC64;

Query Match 13.5%; Score 283.5; DB 1; Length 559;
Best Local Similarity 29.5%; Pred. No. 3.3e-16;
Matches 80; Conservative 43; Mismatches 107; Indels 41; Gaps 8;

QY 40 DGKDIPQASLVFDVALLDL---HNPKDLSIENKVVENCER-----ISQSGDF 86
Db 3 DDFDIPAGDDMMGDMGDFGAGPGMKVGEENEIGKQGLKKLLKSGEGWDTPEVGDE 62
QY 87 LRHYNGTLLDGLTFDSSYSNRRTFTDVIQGYVIPGMDGLGVCIGEKRIIVVPHLHG 146
Db 63 VEVHYTGTLGKFKFSRDRDFTFKLQGGQVIGKWDQGIKTMKGGENALFTTIPPELA 122
QY 147 YGEGR-GNIPGSVAVLFDIHDVFNHPSDSISITSHYKPPDCSVLSKKGD----- 196
Db 123 YGESGSPPTIPANATLQFDVLELLSWTSVDTAKGGIFKK-----ILKGDKNWPKDPD 177
QY 197 --YLYKHYNASLLDGLTLLDSTWNLGKTYNIVLGSQVVLGMDMGLEMCVGEKRTVIIPP 254
Db 178 EVFVK--YEARLEDGTIVSVKS---EGVEFTVKDGHLCALAKAVKTMKGKVLAVKP 231
QY 255 HLGYGE-----AGVDGEVPGSAVLVFDIELL 280
Db 232 QYGFGEGRPAAGEGGAVPPNASLVLDLELV 262

RESULT 3
FKB2 MOUSE
ID FKB2_MOUSE STANDARD; PRT; 140 AA.
AC F45878;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)

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FT VARIANT 21 21 S -> TA.
FT FT /FTid=VAR_006410.
FT VARIANT 24 24 T -> A.
FT FT /FTid=VAR_006411.
FT VARIANT 96 96 Y -> C.
FT FT /FTid=VAR_006412.
SQ SEQUENCE 141 AA; 15654 MW; 9F4751CA7D82D064 CRC64;

Query Match 11.2%; Score 236.5; DB 1; Length 141;
Best Local Similarity 46.7%; Pred.No. 4.9e-13;
Matches 50; Conservative 18; Mismatches 36; Indels 3; Gaps 2;

Qy 63 KDSISIKNVKVPENCERISQSGDLRYHYNGTLLDGLTDFSSYSNRRTFTYIGQGYVIP 122
Db 29 KLQIGVKKRV--DHCPIKSRKGDVLHMHYTKLEDTGTFEDSSLPQNPQFPVFLGTGVQVIK 85

Qy 123 GWDEGLLGVICGEKRIIVPPHGLYGEGR-GNIPGSAVLVFDIHI 168
Db 87 GWDQGLLGVYGEKRLKLVIPSELGYGERGAPPKIPGGATLVFEVELL 133

RESULT 6
FK21_NEUCR STANDARD; PRT; 217 AA.
ID FK21_NEUCR AC O60046;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE FK506-binding protein precursor (FKBP-21) (Peptidyl-prolyl cis-
trans isomerase) (PPIase) (EC 5.2.1.8).
GN FKBP-21.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OC NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=74-OR23-1A;
RA Solscheid B. Tropschug M.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (Potential).
CC -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.

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or send an email to license@isb-sib.ch).
-----
CC EMBL; AJ006297; CAA06962.1; --
CC HSP; Q00688; 1PBK.
DR InterPro; IPR000886; ER target.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00254; FKBP; 1.
DR PROSITE; PS00453; FKBP_PPIASE_1; FALSE_NEG.
DR PROSITE; PS00454; FKBP_PPIASE_2; 1.
DR PROSITE; PS00059; FKBP_PPIASE_3; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
KW isomerase; Rotamase; Signal; Endoplasmic reticulum; Multigene family.
FT SIGNAL 1 20
FT CHAIN 21 217 FK506-BINDING PROTEIN.
FT SITE 214 217 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 217 AA; 22915 MW; 72313067521BCDAF CRC64;

Query Match 11.1%; Score 233.5; DB 1; Length 217;
Best Local Similarity 46.4%; Pred.No. 1.5e-12;
Matches 45; Conservative 15; Mismatches 36; Indels 1; Gaps 1;

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Best Local Similarity 29.8%; Pred. No. 7e-09; Matches 64; Conservative 35; Mismatches 80; Indels 36; Gaps 9;

QY 84 GDFLRHYNGTLLDGTLDSTWNLGKTYN---IVLGSQO---VVLGMDMGLREMGV 245
 Db 50 GDKVYHYKGLMSDGKPKFSDSHDRKPEAFSLGQGVKAWDVGSTMKKEICHLCKP 109
 QY 144 HLGVEGER-GNIPGSVAVLVDIHDVFNHP---SDSISIT-----SHYKPPDCSVLSK 193
 Db 110 EYAGSGHGLQKIPSNATLFPFIEILLDPKGBDLFSDSGVIRIKRKGEGYSNPN-----163
 QY 194 KGYLYKHYNASLIDGTLLDSTWNLGKTYN---IVLGSQO---VVLGMDMGLREMGV 245
 Db 164 EGATVKVH-----LEGCC-----GRTFDCRDVVVVGEGEDHDIPIDIGIDKALVQORE 212
 QY 246 EKRTVIIPHLGYEAGVDG-EVPGSAVLVDIEL 279
 Db 213 EQCILVLPYRGEGAGKPKFGIDPNAEIMYEVL 247

RESULT 9

FKB3_HUMAN
 ID FKB3_HUMAN STANDARD; PRT; 457 AA.
 AC Q13451;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUN-2002 (Rel. 36, Last sequence update)
 DE 51 kDa FK506-binding protein (FKBP51) (Peptidyl-prolyl cis-trans isomerase) (EC 5.2.1.8) (PPIase) (Rotamase) (54 kDa progesterone receptor-associated immunophilin) (FKBP54) (P54) (PFI antigen) (HSP90-binding immunophilin) (Androgen-regulated protein 6).
 DE FKBP5 OR AIG6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RP TISSUE=Thymus;
 RC MEDLINE=97242207; PubMed=9125197;
 RA Baughman G., Wiederrecht G.J., Chang F., Martin M.M., Bourgeois S.;
 RT "Tissue distribution and abundance of human FKBP51, an FK506-binding protein that can mediate calcineurin inhibition.";
 RL Biochem. Biophys. Res. Commun. 232:437-443 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Zhang J.S., Smith D.I.;
 RT "Identification of AIG6 as an androgen response gene in human prostate cancer cell line LNCaP.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 9-457 FROM N.A.
 RX MEDLINE=97154494; PubMed=9001212;
 RA Nair S.C., Rimerman R.A., Toran E.J., Chen S., Prapapanich V.,
 RA Butts R.N., Smith D.F.;
 RT "Molecular cloning of human FKBP51 and comparisons of immunophilin interactions with Hsp90 and progesterone receptor.";
 RL Mol. Cell. Biol. 17:594-603 (1997).
 RN [4]
 RP CHARACTERIZATION.
 RX MEDLINE=94043261; PubMed=7693698;
 RA Smith D.F., Albers M.W., Schreiber S.L., Leach K.L., Deibel M.R. Jr.;
 RA "FKBP54, a novel FK506-binding protein in avian progesterone receptor complexes and HeLa extracts";
 RL J. Biol. Chem. 268:24270-24273 (1993).
 CC -!- FUNCTION: INTERACTS WITH FUNCTIONALLY MATURE HETERO-OLIGOMERIC
 CC PROGESTERONE RECEPTOR COMPLEXES ALONG WITH HSP90 AND P23.
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 CC PEPTIDE BONDS IN OLIGOPETIDES.
 CC -!- ENZYME REGULATION: INHIBITED BY FK506 BUT NOT CYCLOSPORIN.
 CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
 CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED, ENRICHED IN TESTIS COMPARED
 CC TO OTHER TISSUES.

CC -!- INDUCTION: By androgen.
 CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS 2
 CC FKBP-LIKE DOMAINS.
 CC -!- SIMILARITY: CONTAINS 3 TPR REPEATS.
 CC
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 CC
 CC EMBL; U71321; AAC51189.1; -.
 CC EMBL; AF194172; AAL54872.1; -.
 CC EMBL; U42031; AAA86245.1; -.
 CC HSP; P27124; 1ROT.
 CC Genew; HGNC:3721; FKBP5.
 CC MIM; 602623; -.
 CC InterPro; IPR001179; FKBP_PPIase.
 CC InterPro; IPR001440; TPR.
 CC Pfam; PF00254; FKBP; 2.
 CC Pfam; PF00515; TPR; 2.
 CC PROSITE; PS00453; FKBP_PPIASE_1; 1.
 CC PROSITE; PS00454; FKBP_PPIASE_2; 1.
 CC PROSITE; PS00509; FKBP_PPIASE_3; 2.
 CC Isomerase; Rotamase; TPR repeat; Repeat; Nuclear protein.
 FT DOMAIN 42 130 PPIASE, FKBP-TYPE 1.
 FT DOMAIN 157 243 PPIASE, FKBP-TYPE 2.
 FT REPEAT 268 301 TPR 1.
 FT REPEAT 317 350 TPR 2.
 FT REPEAT 352 384 TPR 3.
 SQ SEQUENCE 457 AA; 51212 MW; 18A86608C6891A73 CRC64;
 Query Match 9.2%; Score 194; DB 1; Length 457;
 Best Local Similarity 26.1%; Pred. No. 8.5e-09;
 Matches 67; Conservative 37; Mismatches 85; Indels 68; Gaps 9;
 QY 58 DLNPKDS--ISIKNVVPCERISQDFLYHYNGTLLDGTLDSTWNLGKTYN---115
 Db 24 DITSKDRGLVKIKRV--GNGETPMIGDKVYHYKGLSKGKFKDSSDRNEPVSFL 81
 QY 116 GQGVVPGWDEGLGVCIGEKRIWVPHLYGEGR-GNIPGSVAVLVDIHDVFNHP 174
 Db 82 GKGVKAMDIGVATMKKGICHLCKPEYAGSAGSLPKIPSNATLFPFIEILLDF---137
 QY 175 DSISITSHVKKPPDCSVLSKKGDKLYKHYNASLIDGTLLDSTWNLGKTYN---223
 Db 138 -----KGEDL-----FEGGIIRTRKRGEGYSNPNEGATVEIH 171
 QY 224 -----IVLGSQO---VVLGMDMGLREMGVCKRTVIIPHLGYEAGVD 264
 Db 172 LEGRCGRMPDCRDVAVTVGEGEDHDIPIDIGIDKALEKMQREEQCTILVLPYRGEGAGK 231
 QY 265 --GEVPGSAVLVDIEL 279
 Db 232 KFGIEP-NAELIYEVL 247
 RESULT 10
 FKB3_ARATH
 ID FKB3_ARATH STANDARD; PRT; 208 AA.
 AC Q9SCY2;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Probable FKBP-type peptidyl-prolyl cis-trans isomerase 3, chloroplast
 DE precursor (EC 5.2.1.8) (Ppiase) (Rotamase).
 GN FKBK OR AT5G45680 OR MRA19.7.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.

OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=98403884; PubMed=9734815;
 RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
 RT Sequence features of the regions of 1,367,185 bp covered by 19
 RT physically assigned P1 and TAC clones.";
 RL DNA Res. 5:203-216(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "Riken Arabidopsis full length cDNA clones (RAFTs) sequenced by the
 RT SSP consortium (Salk/Stanford/PGEC).";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 101-176 FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Kolkisaoglu U., Billion K., Eckhoff A., Moeller A., Saal B.,
 RA Wanke D., Schulz B.;
 RT "Structure and evolution of FKBP-like genes in Arabidopsis.";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 80-99.
 RC STRAIN=cv. Columbia;
 RA Kieselbach T., Petersson U., Bystedt M., Schroeder W.P.;
 RL Submitted (JAN-2000) to the SWISS-PROT data bank.
 CC -1- FUNCTION: PPIases accelerate the folding of proteins. It catalyzes
 CC the cis-trans isomerization of proline imidic peptide bonds in
 CC oligopeptides (by similarity).
 CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega-180) = peptidylproline
 CC (omega=0).
 CC -1- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
 CC -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; AB012245; BAB09210.1; -;
 DR EMBL; AY065047; AAL57682.1; -;
 DR EMBL; AJ242483; CAB64723.1; -;
 DR HSSP; P20081.1VAT.
 DR InterPro; IPR001179; FKBP_PPIase.
 DR Pfam; PF00254; FKBP; 1.
 DR ProDom; PD001516; FKBP_Nterm; 1.
 DR PROSITE; PS00453; FKBP_PPIASE_1; 1.
 DR PROSITE; PS00454; FKBP_PPIASE_2; 1.
 DR PROSITE; PS00059; FKBP_PPIASE_3; 1.
 KW Isomerase; Rotamase; Chloroplast; Thylakoid; Transit peptide.
 FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
 FT CHAIN 79 THYLAKOID.
 FT DOMAIN 80 208 PROBABLE FKBP-TYPE PEPTIDYL-PROLYL CIS-
 FT TRANS ISOMERASE 3.
 FT SEQUENCE 208 AA; 22039 MW; 4E6640FE7955A48F CRC64;
 Query Match 9.2%; Score 193; DB 1; Length 208;
 Best Local Similarity 35.3%; Pred. No. 3.7e-09;
 Matches 49; Conservative 23; Mismatches 45; Indels 22; Gaps 5;
 QY 52 FDVALLD-LHNPKDSISNKKVPPEN---CERI-----SQSGDFLRHYNGTLLDGTFL 101
 DB 67 FSIGLDNLVSALETSCFSFSPSGLAFCDKVGVGPEAVKQLIKAHVGLKNGKVF 126
 QY 102 DSSYSRNTFTDYIGGYVPGMDEGLLG-----VCIGEKRIIVPPHLYGEEGRG-- 153
 DB 127 DSSYNRGKPLTPRIGVGVIKWDQILGSDGIPPLMTGKRTLRIPPELAYGDRGAGCK 186

QY 154 ----NIPSAVLVFDHVI 168
 DB 187 GGSCLIPPASVLLFDIEYI 205
 RESULT 11
 ID FKBA_AERHY STANDARD; PRT; 268 AA.
 AC O08437;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE FKBP-type peptidyl-prolyl cis-trans isomerase fkpa precursor
 DE (EC 5.2.1.8) (PPIase) (Rotamase).
 GN FKPA.
 OS Aeromonas hydrophila.
 OC Bacteria; Proteobacteria; gamma subdivision; Aeromonadaceae;
 OC Aeromonas.
 OX NCBI_TaxID=644;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A6;
 RX MEDLINE=97315206; PubMed=9171380;
 RA Wong C.Y.F., Heuzenroeder M.W., Quinn D.M., Flower R.L.P.;
 RT "Cloning and characterization of two immunophilin-like genes, ilpA and
 RT fkpa, on a single 3.9-kilobase fragment of Aeromonas hydrophila
 RT genomic DNA.";
 RL J. Bacteriol. 179:3397-3403(1997).
 CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS. FKPA
 CC PROBABLY ACTS IN THE FOLDING OF EXTRACYTOSOLIC PROTEINS.
 CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -1- SUBCELLULAR LOCATION: Periplasmic (by similarity).
 CC -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; U56832; AAC45362.1; -;
 DR HSSP; P20071.1FKJ.
 DR InterPro; IPR000774; FKBP_Nterm.
 DR InterPro; IPR001179; FKBP_PPIase.
 DR Pfam; PF00254; FKBP; 1.
 DR Pfam; PF01346; FKBP_N; 1.
 DR ProDom; PD001516; FKBP_Nterm; 1.
 DR PROSITE; PS00453; FKBP_PPIASE_1; 1.
 DR PROSITE; PS00454; FKBP_PPIASE_2; 1.
 DR PROSITE; PS00059; FKBP_PPIASE_3; 1.
 KW Isomerase; Rotamase; Periplasmic; Signal.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 268 FKBP-TYPE PEPTIDYL-PROLYL CIS-TRANS
 FT ISOMERASE FKPA.
 FT DOMAIN 172 257 PPIASE, FKBP-TYPE.
 FT SEQUENCE 268 AA; 28685 MW; 5E88D74A830BE3FA CRC64;
 Query Match 9.0%; Score 190; DB 1; Length 268;
 Best Local Similarity 43.3%; Pred. No. 9.1e-09;
 Matches 39; Conservative 14; Mismatches 35; Indels 2; Gaps 1;
 QY 85 DFLRYHYNGTLLDGTFLDSSYSRNTFTDYIGQGYVPGMDEGLLGVCIGEKRIIVVPPH 144
 DB 173 DIVKHYVTGTLTDTGTFDSSVDRGPATFPLNQ--VIPGWTEGVQLMPVGSKFPLPSK 230
 QY 145 LGVGEGRGNIPGSANVLVFDHVIDFNPS 174
 DB 231 LAYGEHAGSIPANANVLVFDVELLAIEKPA 260

[illegible]

(p)ase (EC 5.2.1.8) (Rapamycin-binding protein).
 FPR1 OR FKB1 OR RBP1 OR YNL135C OR N1213 OR N1845.
 Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91126049; PubMed=1704127;
 RA Wiederrecht G.J., Brizuela L., Ellison K.O., Sigal N.H.,
 RT Siekierka J.J.;
 RT "FKB1 encodes a nonessential FK 506-binding protein in Saccharomycetes
 RT cerevisiae and contains regions suggesting homology to the
 RT cyclophilins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:1029-1033(1991).
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91156723; PubMed=1705713;
 RA Heitman J., Novva R.N., Hiestand P.C., Hall M.N.;
 RT "FK 506-binding protein proline rotamase is a target for the
 RT immunosuppressive agent FK 506 in Saccharomycetes cerevisiae.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:1948-1952(1991).
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91141524; PubMed=1996117;
 RA Koltin Y., Faucette L., Bergsma D.J., Levy M.A., Cafferkey R.,
 RA Koser P.L., Johnson R.K., Livi G.P.;
 RA "Rapamycin sensitivity in Saccharomycetes cerevisiae is mediated by a
 RT peptidyl-prolyl cis-trans isomerase related to human FK506-binding
 RT protein.";
 RL Mol. Cell. Biol. 11:1718-1723(1991).
 RN
 RP SEQUENCE FROM N.A.
 RX STRAIN=S288C;
 RA Mallet L., Bussereau F., Jacquet M.;
 RA "A 43.5 kb segment of yeast chromosome XIV, which contains MPA2,
 RT MFP2, CAP/SRV2, NAM9, FKBI/FPR1/RBP1, MOM22 and CPT1, predicts an
 RT adenosine deaminase gene and 14 new open reading frames.";
 RL Yeast 11:1195-1209(1995).
 RN
 RP SEQUENCE OF 67-100.
 RX MEDLINE=91065908; PubMed=1701173;
 RA Siekierka J.J., Widerrecht G., Greulich H., Boulton D., Hung S.H.Y.,
 RA Cryan J., Hodges P.J., Sigal N.H.;
 RA "The cytosolic-binding protein for the immunosuppressant FK-506 is
 RT both a ubiquitous and highly conserved peptidyl-prolyl cis-trans
 RT isomerase.";
 RL J. Biol. Chem. 265:21011-21015(1990).
 RN
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=93216714; PubMed=7681823;
 RA Rotonda J., Burbaum J.J., Chan H.K., Marcy A.I., Becker J.W.;
 RT "Improved calcineurin inhibition by yeast FKBP12-drug complexes.
 RT Crystallographic and functional analysis.";
 RL J. Biol. Chem. 268:7607-7609(1993).
 CC
 CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
 CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- MISCELLANEOUS: FKBP BINDS TO THE IMMUNOSUPPRESSANT DRUG FK506 AND
 CC ALSO MEDIATES THE SENSITIVITY TO RAPAMYCIN.
 CC
 CC -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
 CC
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 CC
 CC EMBL; Z46843; CAA86890.1; -

DR EMBL; M57967; AAA03564.1; -
 DR EMBL; M60877; AAA34607.1; -
 DR EMBL; M63892; AAA34962.1; -
 DR EMBL; Z71411; CAA96017.1; -
 DR PIR; A31146; A33146.
 DR PIR; A37870; A37870.
 DR PIR; A39122; A39122.
 DR PIR; C38333; C38333.
 DR PIR; S13758; S13758.
 DR PDB; 1YAT; 3I-OCT-93.
 DR SGD; S0005079; FPR1.
 DR InterPro; IPR001179; FKBP_PPIase.
 DR Pfam; PF00254; FKBP; 1.
 DR PROSITE; PS00453; FKBP_PPIASE_1; 1.
 DR PROSITE; PS00454; FKBP_PPIASE_2; 1.
 DR PROSITE; PS00509; FKBP_PPIASE_3; 1.
 KW Isomerase; Rotamase; 3D-structure.
 FT STRAND 3 4
 FT HELIX 6 8
 FT STRAND 10 15
 FT TURN 25 26
 FT STRAND 28 37
 FT TURN 38 39
 FT STRAND 42 45
 FT TURN 47 50
 FT STRAND 53 56
 FT TURN 57 58
 FT HELIX 64 72
 FT TURN 75 76
 FT STRAND 78 83
 FT HELIX 85 87
 FT TURN 88 92
 FT STRAND 94 94
 FT TURN 95 97
 FT STRAND 98 98
 FT TURN 100 101
 FT STRAND 104 113
 FT TURN 114 114
 SQ SEQUENCE 114 AA; 12158 MW; 65C134830D300C06 CRC64;
 Query Match 8.9%; Score 188; DB 1; Length 114;
 Best Local Similarity 36.2%; Pred. No. 4.4e-09;
 Matches 42; Conservative 22; Mismatches 46; Indels 6; Gaps 1;
 QY 167 VIDFHPNDSISITSHYKPPDCSVLSKKGVLYKHYNASLDGLTLLSTWNLGKTYNIVL 226
 DB 4 VIGNWKIDRIS-----PDGATFPKTGDLVTHTYGTLENGKQFSSVDGSPFCQNI 57
 QY 227 GSGQVVLGMDMLRECMVGEKRTVIIPHLGYGEAGVDGEVPGSAVLVFDLLEL 282
 DB 58 GVGQVIKGDVGIKLSVGEKARLTIPYAYGPRGFLIPNSTLVFDVLELLKV 113
 RESULT 14
 FKB4 HUMAN STANDARD; PRT; 458 AA.
 AC Q02750; Q9UCV7; Q9UCPI;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE FK506-binding protein 4 (possible peptidyl-prolyl cis-trans isomerase
 DE DE FKB4) (EC 5.2.1.8) (PPIase) (Rotamase) (p59 protein) (HSP binding
 DE immunophilin) (HBI) (FKBP52 protein) (52 kDa FK506 binding protein)
 DE (FKBP59).
 GN FKB4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
 RC TISSUE=Placenta;
 RX MEDLINE=93066366; PubMed=1279700;
 RA Peattie D.A., Harding M.W., Fleming M.A., Decenzo M.T.,

RA Lippe J.A., Livingston D.J., Benasutti M.;
RT "Expression and characterization of human FKBP52, an immunophilin
RT that associates with the 90-kDa heat shock protein and is a component
RT of steroid receptor complexes.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:10974-10978(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung, Lymph, and Uterus;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 1-24, SUBUNIT, AND FUNCTION.
RC TISSUE=Thymus;
RA MEDLINE=92285692; PubMed=1376003;
RX Tai P.-K.K., Albers M.W., Chang H., Faber L.E., Schreiber S.L.;
RT "Association of a 59-kilodalton immunophilin with the glucocorticoid
RT receptor complex.";
RL Science 256:1315-1318(1992).
RN [4]
RP SEQUENCE OF 1-20, FUNCTION, SUBUNIT, AND SUBCELLULAR LOCATION.
RC TISSUE=Lymphocytes;
RX MEDLINE=90335311; PubMed=2378870;
RA Sanchez E.R., Faber L.E., Henzel W.J., Pratt W.B.;
RT "The 56-59-kilodalton protein identified in untransformed steroid
RT receptor complexes is a unique protein that exists in cytosol in a
RT complex with both the 70- and 90-kilodalton heat shock proteins.";
RL Biochemistry 29:5145-5152(1990).
RN [5]
RP SEQUENCE OF 1-17.
RC TISSUE=T-cell;
RX MEDLINE=92147620; PubMed=1371107;
RA Yem A.W., Tomasselli A.G., Heinrikson R.L., Zurcher-Neely H.,
Ruff V.A., Johnson R.A., Deibel M.R. Jr.;
RT "The Hsp56 component of steroid receptor complexes binds to
RT immobilized FK506 and shows homology to FKBP-12 and FKBP-13.";
RL J. Biol. Chem. 267:2868-2871(1992).
RN [6]
RP FUNCTION: Component of unactivated mammalian steroid receptor
CC complexes that sediment at 8-10 S. May have a rotamase activity.
CC May play a role in the intracellular trafficking of hetero-
CC oligomeric forms of steroid hormone receptors.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SUBUNIT: Associates with HSP90 and HSP70 in unactivated steroid
CC hormone receptor complexes. Also interacts with peroxisomal
CC phytanoyl-coA alpha-hydroxylase (PHYH).
CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED.
CC -!- PTM: Phosphorylation by CK2 results in loss of HSP90 binding
CC activity (By similarity).
CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
CC -!- SIMILARITY: CONTAINS 2 FKBP-TYPE PPIASE DOMAINS.
CC -!- SIMILARITY: CONTAINS 3 TPR REPEATS.
CC
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CC
CC EMBL; M88279; AAA36111.1; -;
CC EMBL; BC001786; AAH01786.1; -;
CC EMBL; BC002887; AAH02887.1; -;
CC EMBL; BC007924; AAH07924.1; -;
CC PIR; A46372; A46372.
CC HSSP; P27124; 1ROT.
CC Genew; HGNC:3720; FKBP4.
CC MIM; 600611; -;
CC InterPro; IPR001179; FKBP_PPIase.
CC InterPro; IPR001440; TPR.
CC Pfam; PF00254; FKBP; 2.
CC Pfam; PF00515; TPR; 3.

DR SMART; SM00028; TPR; 3.
DR PROSITE; PS00453; FKBP_PPIASE_1; 1.
DR PROSITE; PS00454; FKBP_PPIASE_2; 2.
DR PROSITE; PS00509; FKBP_PPIASE_3; 2.
KW Isomerase; Rotamase; Repeat; TPR repeat; Nuclear protein;
KW Phosphorylation.
FT INIT MET 0
FT DOMAIN 49 137 PPIASE, FKBP-TYPE 1.
FT DOMAIN 166 252 PPIASE, FKBP-TYPE 2.
FT REPEAT 269 302 TPR 1.
FT REPEAT 318 351 TPR 2.
FT REPEAT 353 385 TPR 3.
FT MOD_RES 142 142 PHOSPHORYLATION (BY CK2) (BY SIMILARITY).
FT CONFLICT 145 146 ED -> AR (IN REF. 2; AAH02887).
SQ SEQUENCE 458 AA; 51673 MW; 916B3B945C51634E CRC64;
Query Match 8.9%; Score 188; DB 1; Length 458;
Best Local Similarity 27.6%; Pred. No. 2.7e-08;
Matches 58; Conservative 36; Mismatches 92; Indels 24; Gaps 7;
QY 84 GDFLRHYNGTLDGTLFDSSYSRNRTFTYIGQYVPGNDEGLLGVICGEKRRIVVPP 143
DB 49 GDRVFVHYTGWLLDGTGKFDSSLDKDKKFSFDLGKGEVKAWDIAIATMKVGEVCHITCKP 108
QY 144 HLGYGEGGR-GNIPGSAVLVFDIHVIDFH-----NPDSISI-----TSHYKPPDCSV 190
DB 109 EVAYGAGSGPPKTPPNATLVFEVLFEGKEDLTEEDGGIIRIQTREGYAKNEGAI 168
QY 191 LSKKGYLYKHYNASLLDGTLLTWNLGTNTYIVLGSQGVVLGMDMLGRLMVCGEKRTV 250
DB 169 VEVA---LEGYKDKLFDQREL--RFEIGEGENL-----DLPGYGLERAIQRMKEGHSIV 218
QY 251 ITPPHLGYGEAGVDG-EVPGSAVLVFDIEL 279
DB 219 YLKPSYAFSGVGKFKQIPPNALKEYLHL 248
RESULT 15
FKBP_DROME STANDARD; PRT; 108 AA.
ID FKBP_DROME STANDARD; PRT; 108 AA.
AC P48375;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 12 kDa FK506-binding protein (FKBP) (Peptidyl-prolyl cis-trans
DE isomerase) (PPIase) (EC 5.2.1.8) (Macrolide binding protein).
GN FK506-BP2 OR FKBP12.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Canton-S; TISSUE=Head;
RA Mounsey A.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Wang T., Li B.Y., Danielson P.D., Shah P.C., Rockwell S.,
RA Lechleider R.J., Martin J., Mangano T., Donahoe P.K.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (potential).
CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
CC
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CC or send an email to license@isb-sib.ch).

DR EMBL; Z49079; CAA88904.1; -;
DR EMBL; U41441; AAA91178.1; -;
DR HSSP; P18203; 1PKL.
DR FlyBase; FBgn013954; FK506-bp2.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00254; FKBP; 1.
DR PROSITE; PS00453; FKBP_PPIASE_1; 1.
DR PROSITE; PS00454; FKBP_PPIASE_2; 1.
DR PROSITE; PS0059; FKBP_PPIASE_3; 1.
KW isomerase; Rotamase.
SQ SEQUENCE 108 AA; 11597 MW; 48BCF993AC8D350A CRC64;

Query Match 8.8%; Score 184.5; DB 1; Length 108;
Best Local Similarity 37.8%; Pred. NO. 8.1e-09;
Matches 37; Conservative 19; Mismatches 41; Indels 1; Gaps 1;
Qy 72 VVPENCERISQSGDPLRYHYNGTLLDGTLDSSYSRNRTFTVIGQYVIPGMDEGLGV 131
Db 8 IAPGDGSTYPKNGQVTVYHTTGLDDGTGKFDSSRDNRNPKFTIGKGEVIRGWDEGVAQL 67
Qy 132 CIGEKRRIVVPPHLGYGEEGR-GNIPGSAVLVFDIHVI 168
Db 68 SVQGSAKLICSPDYAYGSRGHPGVIPPNSTLTDFVELL 105

Search completed: April 26, 2003, 06:56:22
Job time : 8.91662 secs

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OM protein - protein search, using sw model

Run on: April 26, 2003, 06:48:54 ; Search time 34.1369 Seconds

(without alignments)
2341.934 Million cell updates/sec

Title: US-09-225-502-8

Perfect score: 2106

Sequence: 1 TYGEIGWLIPGMDKGLGMC.....VNDPFLKLYFTNLNYFVLM 388

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1623	77.1	517	4	Q95302
2	1585	75.3	570	11	Q92247
3	1585	75.3	570	11	Q9R386
4	1353	64.2	577	13	Q9VIC3
5	1059.5	50.8	564	13	Q9I8P8
6	1022	48.5	581	11	Q9VHI1
7	1000.5	47.5	481	4	Q9H6N5
8	1000.5	47.5	582	4	Q9H3N3
9	1000.5	47.5	582	4	Q96AX3
10	688	32.7	355	4	Q9H6J3
11	572.5	27.2	262	4	Q9UEF9
12	386	18.3	137	13	Q98UD7
13	353.5	16.8	261	5	Q16309
14	344	16.3	264	5	P91180
15	344	16.3	300	5	Q95Q60
16	301.5	14.3	259	5	Q23338

17	287	13.6	216	5	Q9V3V2
18	286.5	13.6	139	5	Q20107
19	285	13.5	216	5	Q9XZ54
20	275	13.1	138	5	Q9VGK3
21	274	13.0	578	10	Q9FJL3
22	272.5	12.9	209	5	Q966Y5
23	269.5	12.8	312	2	Q53919
24	269	12.8	151	10	Q41649
25	265.5	12.6	163	10	Q9FJL2
26	265.5	12.6	163	10	Q38936
27	262	12.4	304	5	Q9XW05
28	259	12.3	146	10	Q38935
29	259	12.3	153	10	Q9LSF4
30	256.5	12.2	134	5	Q17280
31	251.5	11.9	551	10	Q38931
32	251.5	11.9	551	10	Q38949
33	251.5	11.9	555	10	Q9LSF3
34	250.5	11.9	568	10	O04843
35	247.5	11.8	142	4	Q9BTS7
36	237.5	11.3	137	5	Q96335
37	234.5	11.1	211	4	Q9NWM8
38	227.5	10.8	119	13	Q9DFL8
39	225.5	10.7	198	11	Q9CRE4
40	225	10.7	222	4	Q9Y6B0
41	225	10.7	222	4	Q96DA4
42	223.5	10.6	189	11	Q9D8P8
43	223.5	10.6	201	11	Q9D1M7
44	221.5	10.5	201	4	Q9NYL4
45	214.5	10.2	113	16	Q9HXS4

ALIGNMENTS

RESULT 1

Q95302 PRELIMINARY; PRT; 517 AA.

AC Q95302; Q96IJ9; Q96EX5; DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE FK506 binding protein 9 (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (Fragment).
GN FKBP9 OR FKBP63.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99453729; PubMed=10524204;
RA Shadidy M., Caubit X., Olsen R., Seternes O.M., Moens U., Krauss S.;
RT "Biochemical analysis of mouse FKBP60, a novel member of the FKBP family."
RL Biochim. Biophys. Acta 1446:295-307(1999).
RN [2]
RP SEQUENCE OF 317-517 FROM N.A.
RC TISSUE=KIDNEY, AND MUSCLE;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS DURING PROTEIN SYNTHESIS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- ENZYME REGULATION: INHIBITED BY FK506 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -!- PTM: PHOSPHORYLATED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS 4 FKBP-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
DR EMBL; AF089745; AAC78853.1; -;
DR EMBL; BC007443; AA07443.1; -;
DR EMBL; BC011872; AA011872.1; -;

Q9V3V2	drosophila
Q20107	caenorhabdi
Q9XZ54	drosophila
Q9VGK3	drosophila
Q9FJL3	arabidopsis
Q966Y5	suberites d
Q53919	streptomyce
Q41649	vicia faba
Q9FJL2	arabidopsis
Q38936	arabidopsis
Q9XW05	caenorhabdi
Q38935	arabidopsis
Q9LSF4	arabidopsis
Q17280	botryllus s
Q38931	arabidopsis
Q38949	arabidopsis
Q9LSF3	arabidopsis
O04843	triticum ae
Q9BTS7	homo sapien
Q96335	brugia mala
Q9NWM8	homo sapien
Q9DFL8	gillichthys
Q9CRE4	mus musculu
Q9Y6B0	homo sapien
Q96DA4	homo sapien
Q9D8P8	mus musculu
Q9D1M7	mus musculu
Q9NYL4	homo sapien
Q9HXS4	pseudomonas

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DR HSP; P20081; 1YAT.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR000886; ER_target.
DR InterPro: IPR001179; FKBP_PPIase.
DR Pfam: PF00036; ehand; 2.
DR Pfam: PF00254; FKBP; 4.
DR SMART; SM00054; EPH; 2.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00453; FKBP_PPIASE_1; FALSE_NEG.
DR PROSITE; PS00454; FKBP_PPIASE_2; 3.
DR PROSITE; PS00059; FKBP_PPIASE_3; 4.
KW isomerase; Rotamase; Repeat; Glycoprotein; Phosphorylation;
KW Endoplasmic reticulum; Calcium-binding.
FT NON_TER 1
FT DOMAIN 1 86 PPIASE, FKBP-TYPE 1.
FT DOMAIN 105 198 PPIASE, FKBP-TYPE 2.
FT DOMAIN 216 309 PPIASE, FKBP-TYPE 3.
FT DOMAIN 328 421 PPIASE, FKBP-TYPE 4.
FT CA_BIND 439 467 EF-HAND 1 (POTENTIAL).
FT CA_BIND 484 510 EF-HAND 2 (POTENTIAL).
FT SITE 514 517 PREVENT SECRETION FROM ER (POTENTIAL).
FT CARBOHYD 121 121 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 233 233 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 249 249 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 344 344 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 317 319 SIS -> HEG (IN REF. 2; AAH07443).
FT CONFLICT 514 514 H -> Q (IN REF. 2; AAH11872).
SQ SEQUENCE 517 AA; 57219 MW; 704FB0CB9C44C74B CRC64;

Query Match 77.1%; Score 1623; DB 4; Length 517;
Best Local Similarity 99.0%; Pred. No. 5.6e-130;
Matches 305; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TYVEIGWLPMDKGLLGMVCGEKRIITIPPTAYAGDGDGKDIPGQASLVDFVALLDLH 60
Db 142 ITVVGILWLPMDKGLLGMVCGEKRIITIPPTAYAGDGDGKDIPGQASLVDFVALLDLH 201

Qy 61 NPKDSISIKNVVPCNERISQSGDFLRYHYNGTLLDGTLPDSSYSRNRFTDTYIGQGV 120
Db 202 NPKDSISIKNVVPCNERISQSGDFLRYHYNGTLLDGTLPDSSYSRNRFTDTYIGQGV 261

Qy 121 IPGMDGLLGVCIGEKRIIVPPHLYGEGRGNIPGSALVFDIHDVDFNPDSISIT 180
Db 262 IPGMDGLLGVCIGEKRIIVPPHLYGEGRGNIPGSALVFDIHDVDFNPDSISIT 321

Qy 181 SHYKPPDCSVLSKKGYLYKYHNASLLDGTLLDSTWNLGKTYNIVLGGQVVLGMDMGLR 240
Db 322 SHYKPPDCSVLSKKGYLYKYHNASLLDGTLLDSTWNLGKTYNIVLGGQVVLGMDMGLR 381

Qy 241 EMCVGEKRTVIIPHLGYGAGVDGVPGSALVFDIELLELVLGPEGYFVWNGEVSP 300
Db 382 EMCVGEKRTVIIPHLGYGAGVDGVPGSALVFDIELLELVLGPEGYFVWNGEVSP 441

Qy 301 NLFEEINK 308
Db 442 NLFEEIDK 449

RESULT 2
Q92247
ID Q92247 PRELIMINARY; PRT; 570 AA.
AC Q92247; Q9JHX5; Q9CVMO;
DT 01-MAY-1999 (TRENDELrel. 10, Created)
DT 01-MAY-1999 (TRENDELrel. 10, Last sequence update)
DT 01-MAR-2002 (TRENDELrel. 20, Last annotation update)
DE FK506 binding protein 9 precursor (EC 5.2.1.8) (Peptidyl-prolyl cis-
DE trans isomerase) (PPIase) (Rotamase) (FKBPp65RS).
GN* FKBP9 OR FKBP63.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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RN [1]
RP SEQUENCE FROM N.A., ENZYME REGULATION, SUBCELLULAR LOCATION, TISSUE
RP SPECIFICITY, DEVELOPMENTAL STAGE, AND CALCIUM-BINDING ACTIVITY.
RX MEDLINE=99453729; PubMed=10524204;
RT Shadidy M., Caubit X., Olsen R., Seternes O.M., Moens U., Krauss S.;
RT "Biochemical analysis of mouse FKBP60, a novel member of the FKBP
RT family.";
RL Biochim. Biophys. Acta 1446:295-307(1999).
RN [2]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=THYMUS;
RX PubMed=11710534;
RA Jo D., Lyu M.S., Cho B.-G., Park D., Kozak C.A., Kim M.G.;
RA "Identification and genetic mapping of the mouse Fkbp9 gene encoding a
RT new member of FK506-binding protein family.";
RT Mol. Cells 12:272-275(2001).
RN [3]
RP SEQUENCE OF 155-570 FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guscinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mommaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS DURING
CC PROTEIN SYNTHESIS.
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- ENZYME REGULATION: INHIBITED BY FK506.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN HEART, SKELETAL
CC MUSCLE, LUNG, LIVER AND KIDNEY. LOWER LEVELS FOUND IN BRAIN,
CC SPLEEN AND TESTIS.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN ALL DEVELOPMENTAL STAGES.
CC -!- PTM: PHOSPHORYLATED.
CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS 4
CC FKBP-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
DR EMBL; AF090334; AAC72964.1; -
DR EMBL; AF279263; AAF79215.1; -
DR EMBL; AK007499; BAB25071.1; -
DR HSP; P20081; 1YAT.
DR MGD; MGI:1350321; Fkbp9.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR000886; ER_target.
DR InterPro: IPR001179; FKBP_PPIase.
DR Pfam; PF00036; ehand; 2.
DR Pfam; PF00254; FKBP; 4.
DR SMART; SM00054; EPH; 2.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00453; FKBP_PPIASE_1; FALSE_NEG.
DR PROSITE; PS00454; FKBP_PPIASE_2; 3.
DR PROSITE; PS00059; FKBP_PPIASE_3; 4.
KW isomerase; Rotamase; Repeat; Glycoprotein; Signal; Phosphorylation;
KW Endoplasmic reticulum; Calcium-binding.
FT SIGNAL 1 24
FT POTENTIAL.

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FT CHAIN 25 570 FK506 BINDING PROTEIN 9.
FT DOMAIN 45 139 PPIASE, FKBP-TYPE 1.
FT DOMAIN 158 251 PPIASE, FKBP-TYPE 2.
FT DOMAIN 269 362 PPIASE, FKBP-TYPE 3.
FT DOMAIN 381 474 PPIASE, FKBP-TYPE 4.
FT CA_BIND 492 520 EF-HAND 1 (POTENTIAL).
FT CA_BIND 537 563 EF-HAND 2 (POTENTIAL).
FT SITE 567 570 PREVENT SECRETION FROM ER (POTENTIAL).
FT CARBOHYD 174 174 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 302 302 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 397 397 DKG -> NGE (IN REF. 2).
FT CONFLICT 234 236 G -> S (IN REF. 3).
FT CONFLICT 321 321 G -> A (IN REF. 2).
FT CONFLICT 351 351 A -> T (IN REF. 3).
FT CONFLICT 361 361 V -> F (IN REF. 2).
FT CONFLICT 364 364 F -> V (IN REF. 2).
FT CONFLICT 378 378 K -> N (IN REF. 2).
FT CONFLICT 386 386 S -> I (IN REF. 2).
FT CONFLICT 475 475 B -> D (IN REF. 2).
FT CONFLICT 550 550 D -> N (IN REF. 2).
SQ SEQUENCE 570 AA; 62995 MW; DFE8B8F2F6A0FLDA CRC64;

Query Match 75.3%; Score 1585; DB 11; Length 570;
Best Local Similarity 95.8%; Pred. No. 1.1e-126;
Matches 295; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TYGEIGWLIPGMDKGLGCMVGEKRIITIPPPFLAYGEDGDKDIPGQASLVFVALLDLH 60
Db 195 TYVGIGWLIPGMDKGLGCMVGEKRIITIPPPFLAYGEDGDKDIPGQASLVFVALLDLH 254

Qy 61 NPKDSISIEKNKVPENCERISOSGDFLRHYNGTLLDGTLLDSSYSRNRTFTDYIGQYV 120
Db 255 NPKDTISIEKNKVPENCERISOSGDFLRHYNGTLLDGTLLDSSYSRNRTFTDYIGQYV 314

Qy 121 IPGMDGLLVGVCIGEKRRIVVPPHLYGEGEGRNIPGSAVLVDFDIHVIDFHNPSDSISIT 180
Db 315 IPGMDGLLVGVCIGEKRRIVVPPHLYGEGEGRNIPGSAVLVDFDIHVIDFHNPSDSISIT 374

Qy 181 SHYKPPDCSVLSKGDYLYKHYNASLLDGTLLDSTWNLGKTYNIVLGSQVVLGMDMGLR 240
Db 375 SHYKPPDCSVLSKGDYLYKHYNASLLDGTLLDSTWNLGKTYNIVLGSQVVLGMDMGLR 434

Qy 241 EMCVGEKRTVIIPPHLYGEGAGVGEVPGSAVLVDFDIELLELVAGLPEGYMFIMNGEVSP 300
Db 435 EMCVGEKRTVIIPPHLYGEGAGVGEVPGSAVLVDFDIELLELVAGLPEGYMFIMNGEVSP 494

Qy 301 NLFEEINK 308
Db 495 NLFEEIDR 502

RESULT 3
QyR386 PRELIMINARY; PRT; 570 AA.
AC QyR386;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DE FK506 binding protein 9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL: BC026133; AAH26133.1; -. 06AB7BD18786B9D5 CRC64;
SQ SEQUENCE 570 AA; 63014 MW; 06AB7BD18786B9D5 CRC64;

Query Match 75.3%; Score 1585; DB 11; Length 570;

Best Local Similarity 95.8%; Pred. No. 1.1e-126;
Matches 295; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TYGEIGWLIPGMDKGLGCMVGEKRIITIPPPFLAYGEDGDKDIPGQASLVFVALLDLH 60
Db 195 TYVGIGWLIPGMDKGLGCMVGEKRIITIPPPFLAYGEDGDKDIPGQASLVFVALLDLH 254

Qy 61 NPKDSISIEKNKVPENCERISOSGDFLRHYNGTLLDGTLLDSSYSRNRTFTDYIGQYV 120
Db 255 NPKDTISIEKNKVPENCERISOSGDFLRHYNGTLLDGTLLDSSYSRNRTFTDYIGQYV 314

Qy 121 IPGMDGLLVGVCIGEKRRIVVPPHLYGEGEGRNIPGSAVLVDFDIHVIDFHNPSDSISIT 180
Db 315 IPGMDGLLVGVCIGEKRRIVVPPHLYGEGEGRNIPGSAVLVDFDIHVIDFHNPSDSISIT 374

Qy 181 SHYKPPDCSVLSKGDYLYKHYNASLLDGTLLDSTWNLGKTYNIVLGSQVVLGMDMGLR 240
Db 375 SHYKPPDCSVLSKGDYLYKHYNASLLDGTLLDSTWNLGKTYNIVLGSQVVLGMDMGLR 434

Qy 241 EMCVGEKRTVIIPPHLYGEGAGVGEVPGSAVLVDFDIELLELVAGLPEGYMFIMNGEVSP 300
Db 435 EMCVGEKRTVIIPPHLYGEGAGVGEVPGSAVLVDFDIELLELVAGLPEGYMFIMNGEVSP 494

Qy 301 NLFEEINK 308
Db 495 NLFEEIDR 502

RESULT 4
QyVIC3 PRELIMINARY; PRT; 577 AA.
AC QyVIC3;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE CFKBP/SMAP.
GN CFKBP/SMAP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98384310; PubMed-9716519;
RA Fukuda K., Tanigawa Y., Fujii G., Yasugi S., Hirohashi S.;
RT "CFKBP/SMAP, a novel molecule involved in the regulation of smooth
muscle differentiation.";
RL Development 125:3535-3542(1998).
DR EMBL: AB008675; BAA34673.2; -.
DR HSSP; P27124; IROT.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000886; ER target.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00036; ehand; 2.
DR Pfam; PF00254; FKBP; 4.
DR SMART; SM00054; EFh; 2.
DR PROSITE; PS00018; EF HAND; UNKNOWN 1.
DR PROSITE; PS00014; ER TARGET; UNKNOWN 1.
DR PROSITE; PS00454; FKBP_PPIASE 2; UNKNOWN 3.
DR PROSITE; PS00509; FKBP_PPIASE 3; 4.
SQ SEQUENCE 577 AA; 64054 MW; 1E85DEA387AE099B CRC64;

Query Match 64.2%; Score 1353; DB 13; Length 577;
Best Local Similarity 79.7%; Pred. No. 6.9e-107;
Matches 248; Conservative 34; Mismatches 23; Indels 6; Gaps 2;

Qy 1 TYGEIGWLIPGMDKGLGCMVGEKRIITIPPPFLAYGEDGDKDIPGQASLVFVALLDLH 60
Db 200 TYVGIGWLIPGMDKGLGCMVGEKRIITIPPPFLAYGEDGDKDIPGQASLVFVALLDLH 259

Qy 61 NPKDSISIEKNKVPENCERISOSGDFLRHYNGTLLDGTLLDSSYSRNRTFTDYIGQYV 120

Db 260 NPKDGIITENQLVPESECRRTQTGDFIRYHYNGTLLDGTLLFDSSYSRRNRTYDTVVGKGV 319
Qy 121 IPGMDGLGVCIGEKRRIVVPHLGYGEGRGNI PGSAVLVFDIHLVDFHNPDSISIT 180
Db 320 IAGMDEGLGVCIGEKRRIIIPHLGYGEGRGKIPGSAVLVFDIHLVDFHNPDSISIT 379
Qy 181 SHYKPPDCSVLKKGDYLYKHYNASLL--DGTLLDSTWNLGKTYNIVLGSQVVLGMDM 237
Db 380 VNYKPSNCSLLKKGDYLYKHYNASLLGWSASLDTSW---QDLQSSGSGQVVLGMDM 436
Qy 238 GLREMCVGEKRTVIIPHLGYGAGVDEVP GSAVLVFDIHLVDFHNPDSISIT 297
Db 437 GLQDMCVGERRTVIIPHLGYGAGVDEVP GSAVLVFDIHLVDFHNPDSISIT 496
Qy 298 VSPNLFEEINK 308
Db 497 VSPNLFEEIDQ 507

RESULT 5

Q918P8 PRELIMINARY; PRT; 564 AA.
AC Q918P8
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE FK506-binding protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20302564; PubMed=10842073;
RA Spokony R., Saint-Jeannet J.-P.;
RT "Xenopus FK 506-binding protein, a novel immunophilin expressed during
early development.";
RL Mech. Dev. 94:205-208(2000).
DR EMBL; AF232672; AAF35906.1; -.
DR HSSP; P20081; 1YAT.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000886; ER target.
DR Pfam; PF00036; ehand; 2.
DR Pfam; PF00254; FKBP; 4.
DR SMART; SM00054; EFh; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN 1.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN 1.
DR PROSITE; PS00454; FKBP_PPIASE_2; UNKNOWN 2.
DR PROSITE; PS50059; FKBP_PPIASE_3; 4.
SQ SEQUENCE 564 AA; 62643 MW; 15312365BF1E43CF CRC64;

Query Match 50.8%; Score 1069.5; DB 13; Length 564;
Best Local Similarity 58.5%; Pred. No. 1e-82;
Matches 207; Conservative 48; Mismatches 80; Indels 19; Gaps 6;

Qy 1 TYGEIGWLIPGMDKGLLGMVCVGEKRIITIPFLAYGEDGDKDIPGQASLVFVALLDLH 60
Db 186 TVVGSGLWIKGMDGLLGMVCVGEKRIITIPFLAYGEDGDKDIPGQASLVFVALLDLH 245
Qy 61 NPKDSISIEKVVPCNERISQSGDFLRYHYNGTLLDGTLLFDSSYSRRNRTYDTVVGKGV 120
Db 246 NPKDGIITVQNVQVCKKAVTGDYRYHYNGTLLDGTLLFDSSYSRRNRTYDTVVGKGV 305
Qy 121 IPGMDGLGVCIGEKRRIVVPHLGYGEGRGNI PGSAVLVFDIHLVDFHNPDSISIT 179
Db 306 ISGMDAGLQVCVGEKRRIIIPHLGYGEGSGNSIPGSAVLVFDIHLVDFHNPDSISIT 365
Qy 180 TSHYKPPDCSVLKKGDYLYKHYNASLLDGTLLDSTWNLGKTYNIVLGSQVVLGMDMGL 239
Db 366 FVMHKPDCSNTTSKKGDFIKYHCNSMLDGTLLFSSHEYTEPQQVTLGSSKVIKGLDGTGL 425

Qy 240 REMCVGEKRTVIIPHLGYGAGVDEVP GSAVLVFDIHLVDFHNPDSISIT 299
Db 426 LNCVGEKRTVIIPHLAHGEGARG-VPPSAVLKFDLHIEGIPDGFLFWLQDTP 484
Qy 300 PNLFE-----EINKVTF--FCCPFVSWRRWYPEGQ--LPQDSNDSPADL 342
Db 485 ENLFEMDLDKNGEVEPEEFDFLKAQVS-----EGKGRFLPGVDREKSIADM 532

RESULT 6

Q8VHI1 PRELIMINARY; PRT; 581 AA.
AC Q8VHI1
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE 65 kDa FK506-binding protein.
GN FKBP10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Patterson C.E., Gao J., Rooney A.P., Davis E.C.;
RT "Genomic organization of Mouse and Human 65 kDa FK506-binding protein
(FKBP65) genes and evolution of the FKBP Multigene Family.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF456413; AAL57621.1; -.
DR EMBL; AF456412; AAL57621.1; JOINED.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000886; ER target.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00036; ehand; 2.
DR Pfam; PF00254; FKBP; 4.
DR SMART; SM00054; EFh; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN 1.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN 1.
DR PROSITE; PS00454; FKBP_PPIASE_2; UNKNOWN 1.
DR PROSITE; PS50059; FKBP_PPIASE_3; 4.
SQ SEQUENCE 581 AA; 64697 MW; FD6F777940AD91E9 CRC64;

Query Match 48.5%; Score 1022; DB 11; Length 581;
Best Local Similarity 55.8%; Pred. No. 1.2e-78;
Matches 198; Conservative 58; Mismatches 79; Indels 20; Gaps 6;

Qy 1 TYGEIGWLIPGMDKGLLGMVCVGEKRIITIPFLAYGEDGDKDIPGQASLVFVALLDLH 60
Db 202 TVVGSGLWIKGMDGLLGMVCVGEKRIITIPFLAYGEKGYGTVPQASLVFVALLDVH 261
Qy 61 NPKDSISIEKVVPCNERISQSGDFLRYHYNGTLLDGTLLFDSSYSRRNRTYDTVVGKGV 120
Db 262 NPKDVTQLETLELPQGVRRVAVAGDFMRHYNGSLMDGTLLFDSSYSRRNRTYDTVVGQYI 321
Qy 121 IPGMDGLGVCIGEKRRIVVPHLGYGEGRGNI PGSAVLVFDIHLVDFHNPDSISIT 179
Db 322 IPGMDGLQACIGERRITVPPHLYGEGTGDKIPGSAVLVFDIHLVDFHNPDSIPVEI 381
Qy 180 TSHYKPPD-CSVLSKKGDKYLYKHYNASLLDGTLLDSTWNLGKTYNIVLGSQVVLGMDM 238
Db 382 KTLSPENCNETSKIGDFIRHYNCSSLDGTRLFSSHDYEAPOEITLGANKVIEGLDRG 441
Qy 239 LREMCVGEKRTVIIPHLGYGAGVDEVP GSAVLVFDIHLVDFHNPDSISIT 298
Db 442 LQCMCVGERRLIVPPLAHGEGARG-VPPSAVLLEVEVLVSREDGLTGYLFWYQDP 500
Qy 299 SPNLFEEIN-----KVTFECCPFVSWRRWYPEGQ--LPQDSNDSPADL 342
Db 501 SYSLFEDMDLNDKGEVPPPEFDFLKAQVN-----EGKGRIMPQDQDPDKTISDM 549

RESULT 7


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Q9H6N5
ID Q9H6N5 PRELIMINARY; PRT; 481 AA.
AC Q9H6N5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CDNA: FLJ22041.fis, clone HEP09061.
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani T., Ota T., Suzuki Y., Oabayashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RL "NEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
EMBL: AK025694; BAB15220.1; -.
DR HSSP; AK025694; BAB15220.1; -.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000886; ER-target.
DR Pfam; PF00036; ehand; 2.
DR Pfam; PF00254; FKBP; 4.
DR SMART; SM00054; EFN; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
DR PROSITE; PS00454; FKBP_PPIASE_2; UNKNOWN_1.
DR PROSITE; PS00059; FKBP_PPIASE_3; 4.
SQ SEQUENCE 481 AA; 53219 MW; A4D5181BFC88BDFD CRC64;

Query Match 47.5%; Score 1000.5; DB 4; Length 481;
Best Local Similarity 55.1%; Pred. No. 6.2e-77;
Matches 189; Conservative 60; Mismatches 73; Indels 21; Gaps 6;

QY 1 TYGEGWLLIPGMDKGLGCMVGKRIITIPPLAYGEGDGGKIPGQASLVFVALLDLH 60
Db 102 TYVSGWLLIKMGDGLGCMVGKRIITIPPLAYGEGYGTWIPQASLVFVALLIDVH 161
QY 61 NPKDSISTENKVPENCERISQSGDFLYRHYNGTLLDGLTDFSSYSRNRTPDYIGQYV 120
Db 162 NPKDAVQLETLPPGCVRRAGAGDFMRHYNGSLMDGTLPDSSYSRNRHTYNTYIGQYI 221
QY 121 IPGMDGGLGVCIGEKRIIVPPHLYGEGEGRN-IPGSAVLVFDIHFVDFHNPDSISI 179
Db 222 IPGMDGGLGVCIGEKRIIVPPHLYGEGEGRN-IPGSAVLVFDIHFVDFHNPADVVEI 281
QY 180 TSHYKPPD-CVSLSKGDKLYKHYNASLLDGLTLDSTWNLGKTYNIVLGSGQVVLGMDMG 238
Db 282 RTLSRPSETCNETTKLGDVRYHYNGSLMDGTLPDSSYSRNRHTYNTYIGQYI 341
QY 239 LREMCVGEKRTVIIPPHLYGEGAGVDPGSAVLVFDIELLELVAGLPEGYMFIWNGEV 298
Db 342 LQGMCGERRQLIVPPHLAGESGARG-VPGSAVLVFEVLVSREDGLTGYLFWHKDP 400
QY 299 SPNLFE--EINK-----VTFPCFPVSWRRWYPEGSQL 330
Db 401 PANLFEDMDLNKDGVPPEEFTFI-----KAQVSEKGRLL 436

RESULT 8
Q9H3N3
ID Q9H3N3 PRELIMINARY; PRT; 582 AA.
AC Q9H3N3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 65kDa FK506-binding protein.
GN HFKBP65.
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
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OX NCBI_TaxID=9606;
RN [1]
RA SEQUENCE FROM N.A.
RA Ota T., Nishikawa T., Kawai Y., Suzuki Y., Ishii S., Saito K.,
RA Yamamoto J., Sugano S., Isogai T.;
RT "HRI human cDNA sequencing project.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA Mitumori C., Morikawa N., Isogai T., Ota T., Yuri K., Nishikawa T.,
RA Masuho Y., Nagahara K.;
RT "The human 65kDa FK506-binding protein (hFKBP65) gene induces the
RT morphological differentiation of NT2 neuron precursor cells.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
EMBL: AB045981; BAB20974.1; -.
DR HSSP; AB045981; BAB20974.1; -.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000886; ER-target.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00036; ehand; 2.
DR Pfam; PF00254; FKBP; 4.
DR SMART; SM00054; EFN; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
DR PROSITE; PS00454; FKBP_PPIASE_2; UNKNOWN_1.
DR PROSITE; PS00059; FKBP_PPIASE_3; 4.
SQ SEQUENCE 582 AA; 64305 MW; 04B25129A1D4D92 CRC64;

Query Match 47.5%; Score 1000.5; DB 4; Length 582;
Best Local Similarity 55.1%; Pred. No. 8.1e-77;
Matches 189; Conservative 60; Mismatches 73; Indels 21; Gaps 6;

QY 1 TYGEGWLLIPGMDKGLGCMVGKRIITIPPLAYGEGDGGKIPGQASLVFVALLDLH 60
Db 203 TYVSGWLLIKMGDGLGCMVGKRIITIPPLAYGEGYGTWIPQASLVFVALLIDVH 262
QY 61 NPKDSISTENKVPENCERISQSGDFLYRHYNGTLLDGLTDFSSYSRNRTPDYIGQYV 120
Db 263 NPKDAVQLETLPPGCVRRAGAGDFMRHYNGSLMDGTLPDSSYSRNRHTYNTYIGQYI 322
QY 121 IPGMDGGLGVCIGEKRIIVPPHLYGEGEGRN-IPGSAVLVFDIHFVDFHNPDSISI 179
Db 323 IPGMDGGLGVCIGEKRIIVPPHLYGEGEGRN-IPGSAVLVFDIHFVDFHNPADVVEI 382
QY 180 TSHYKPPD-CVSLSKGDKLYKHYNASLLDGLTLDSTWNLGKTYNIVLGSGQVVLGMDMG 238
Db 383 RTLSRPSETCNETTKLGDVRYHYNGSLMDGTLPDSSYSRNRHTYNTYIGQYI 442
QY 239 LREMCVGEKRTVIIPPHLYGEGAGVDPGSAVLVFDIELLELVAGLPEGYMFIWNGEV 298
Db 443 LQGMCGERRQLIVPPHLAGESGARG-VPGSAVLVFEVLVSREDGLTGYLFWHKDP 501
QY 299 SPNLFE--EINK-----VTFPCFPVSWRRWYPEGSQL 330
Db 502 PANLFEDMDLNKDGVPPEEFTFI-----KAQVSEKGRLL 537

RESULT 9
Q96AY3
ID Q96AY3 PRELIMINARY; PRT; 582 AA.
AC Q96AY3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 64.2 kDa protein (65 kDa FK506-binding protein)
DE (EC 5.2.1.8).
GN FKBP65.
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
```

RC TISSUE=BRAIN;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Ruten S., Kinloch R.A., Robinson C., Gettings L., Kay J.E.;
RL "The Human FK506-binding Protein Repertoire";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016467; AAH16467.1; -
DR EMBL; AF337909; AAM15770.1; -
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00036; ehand; 2.
DR Pfam; PF00254; FKBP; 2.
DR SMART; SM0054; EFh; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
DR PROSITE; PS00059; FKBP_PPIASE_3; 4.
DR PROSITE; PS00059; FKBP_PPIASE_3; 4.
KW Hypothetical protein; Isomerase.
SQ SEQUENCE 582 AA; 64245 MW; 98257459158407C2 CRC64;

Query Match 47.5%; Score 1000.5; DB 4; Length 582;
Best Local Similarity 55.1%; Pred. No. 8.1e-77; Indels 21; Gaps 6;
Matches 189; Conservative 60; Mismatches 73;

QY 1 TYGEIGWLIPGMKGLGCMGCGEKRIITIPPPFLAYGEDGDGKDIPQASLAFDVALLDLH 60
DB 203 TYVSGWLIKMGDGLGCMGCGERRKIIPPPFLAYGEGYGVIPQASLAFVHLLIDVH 262

QY 61 NPKDSISIEKNVPCNERISQSGDFLRYHNGTLLDGLTFDSSYSRNRTFTYIGQGVV 120
DB 263 NPKDAVQLETLELPPGCVRRAGAGDFMYHYNGSLMDGLTFDSSYSRNHTYTYIGQYI 322

QY 121 IPGMDEGLLVCIGEKRIIVPPHLYGEGEGRN-IPGSALVDFDIHVDIHNPSDSIGI 179
DB 323 IPGMDQLQACMGERRIIPPHLYGEGTGDKIIPGSALVDFIHNVDIHNPSDVVEI 382

QY 180 TSHYKPPD-CSVLKSGDYLKYHNASLLDGLTSTWNLGTYNIVLGSGQVVLGMDWG 238
DB 383 RTLSRPSSETCNETTKLGDVFRYHYNCSLLDGLTQTFSDYGAPEATLGANKVIEGLDTG 442

QY 239 LREMCVGEKRTVIIPPHLYGEGAGVDGPGSAVLDFDIELELVAGLPEGYMFIWNGEV 298
DB 443 LQGMCGVGERQLIIPPHLAHGESGARG-VPGSAVLDFEVELVSRDGLTGYLFWHKDP 501

QY 299 SPNLFE--EINK-----VTFFCCPFVSWRRWYPEGRGQL 330
DB 502 PANLFEDMDLNKGGEVPEEFSTFI-----KAQVSEKGRGL 537

RESULT 10
Q9H6J3 PRELIMINARY; PRT; 355 AA.
ID Q9H6J3
AC Q9H6J3
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CDNA: FLJ22221 fis, clone HRC01651.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
RA Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
RA Nakamura Y., Isoqai T., Sugano S.;
RT "NEDO human cDNA sequencing Project";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK025874; BAB15266.1; -
DR HSSP; Q00688; 1PBK.

DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00036; ehand; 2.
DR Pfam; PF00254; FKBP; 2.
DR SMART; SM0054; EFh; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
DR PROSITE; PS00059; FKBP_PPIASE_3; 2.
SQ SEQUENCE 355 AA; 38950 MW; DBECF4B8618BF54F CRC64;

Query Match 32.7%; Score 688; DB 4; Length 355;
Best Local Similarity 42.5%; Pred. No. 1.8e-50;
Matches 135; Conservative 50; Mismatches 51; Indels 82; Gaps 6;

QY 87 LRYHYNGTLLDGLTFDSSYSRNRTFTYIGQYVIPGMDEGLLVCIGEKRIIVPPHLYG 146
DB 1 MRYHYNGSLMDGLTFDSSYSRNHTYTYIGQYIIPGMDQLQACMGERRITIPPHLA 60

QY 147 YGEGEGRN----- 154
DB 61 YGEGTDSIGLFGSAPLRFPSRSGEGPSLGRGEGYGTETPAYPODDAVLGASVSPVKW 120

QY 155 -----IPGSALVDFDIHVDIHNPSDSISITSHYKPPD-CSVLKSGDYLKYHN 203
DB 121 ASHADPGDKIPGSALVDFIHNVDIHNVDIHNVDIHNVDIHNVDIHNVDIHNVDIHN 180

QY 204 ASLLDGLTSTWNLGTYNIVLGSGQVVLGMDMGLRMCMVGEKRTVIIPPHLYGEGAGV 263
DB 181 CSLDGLTQTFSDYGAPEATLGANKVIEGLDTGLQGMCGVGERQLIIPPHLAHGESGA 240

QY 264 DGEVPGSAVLDFDIELELVAGLPEGYMFIWNGEVSPNLFE--EINK-----VTFF 312
DB 241 RG-VPGSAVLDFEVELVSRDGLTGYLFWHKDPANLFDMDLNKGGEVPEEFSTFI 299

QY 313 CCPFVSWRRWYPEGRGQL 330
DB 300 -----KAQVSEKGRGL 310

RESULT 11
Q9UF89 PRELIMINARY; PRT; 262 AA.
ID Q9UF89
AC Q9UF89
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 28.9 kDa protein (Fragment).
GN DKFZP586I0821.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=UTERUS;
RA Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL333116; CAB61418.1; -
DR HSSP; Q00688; 1PBK.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00036; ehand; 2.
DR Pfam; PF00254; FKBP; 2.
DR SMART; SM0054; EFh; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
DR PROSITE; PS00059; FKBP_PPIASE_3; 2.
KW Hypothetical protein.
FT NON TER
SQ SEQUENCE 262 AA; 28926 MW; A9630934276BA84E CRC64;

DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE	Hypothetical 29.1 kDa protein.
OS	C50C8.3.
OC	Caenorhabditis elegans.
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC	Rhabditidae; Peloderinae; Caenorhabditis.
OX	NCBI_TaxID=6239;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=BRISTOL N2.
RC	STRAIN=BRISTOL N2;
RA	MEDLINE=99069613; PubMed=9851916;
RX	None;
RT	"Genome sequence of the nematode C. elegans: a platform for
RT	investigating biology. The C. elegans Sequencing Consortium.;"
RL	Science 282:2012-2018(1998).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=BRISTOL N2.
RC	STRAIN=BRISTOL N2;
RA	Sammons L.; Wohldmann P.;
RT	"The sequence of C. elegans cosmid C05C8.1;"
RT	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN	[3]
RP	SEQUENCE FROM N.A.
RC	STRAIN=BRISTOL N2.
RC	STRAIN=BRISTOL N2;
RA	Waterston R.;
RT	"Direct Submission.;"
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF016430; AAB65370.1; -.
DR	HSSP; P27124; IROT.
DR	InterPro; IPR000886; ER target.
DR	InterPro; IPR001179; FKBP_PPase.
DR	Pfam; PF00254; FKBP; 2.
DR	PROSITE; PS00014; ER TARGET; UNKNOWN 1.
DR	PROSITE; PS00454; FKBP_PPASE 2; UNKNOWN 1.
DR	PROSITE; PS50059; FKBP_PPASE_3; 2.
KW	Hypothetical protein.
SQL	SEQUENCE 261 AA; 29080 MW; 545A8B82B1BE26AD CRC64;
Query Match 16.8%; Score 353.5; DB 5; Length 261;	
Best Local Similarity 32.6%; Pred. No. 4e-22;	
Matches 74; Conservative 52; Mismatches 90; Indels 11; Gaps	
Qy	66 ISTENKVVENCERISQSGDFLRHYNGTLLDGTLPDSSYSRNRPTFTYIGQYVPGMD 12
Db	30 IEIIKIGDSKCKIKSESQDLQEQYKLSDEKGVIGSNFQ-QPYTFTLGKGEVIHGME 88
Qy	126 EGIWGVCIEKRIIVPPHILGVGEGRGNIPGSA-VLVFDIHVIDFHP-----SDS 17
Db	89 IAMEGVCVGEQRKVIIPQEQFDEDG-DEVSGKETLYYFVELKSIIPRPGAKWITDEG 14
Qy	177 ISITSHYKPPDCSVLSKGDYIKHYNASLLDGTLLDSTWNLGKTYNVLGSGQVVLGMD 23
Db	148 VHIHTHEVEGTEKAQAGDTTHQOYTYLNLDEGSDIFSWSRNRPFIFKMGSGQVKGMD 20
Qy	237 MGLREMCVCKETVIIPHILGVGAGVDGPGSAVLVFDIELLELV 263
Db	208 IAMEGVCQGEKRVIPPELAYGGRPPAIPGNSYLHFDLSLEKLV 254
RESULT 14	
P91180	
ID	P91180 PRELIMINARY; PRT; 264 AA.
AC	P91180;
DT	01-MAY-1997 (TrEMBLrel. 03, Created)
DT	01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE	Hypothetical 29.9 kDa protein.
GN	C50F2.6.
OS	Caenorhabditis elegans.
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
OC	Rhabditidae; Peloderinae; Caenorhabditis.
OX	NCBI_TaxID=6239;
RN	[1]

